

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:53:06 ; Search time 40.93 Seconds
(without alignments)
1072.116 Million cell updates/sec

Title: US-09-280-567-2
Perfect score: 1634
Sequence: 1 MRALEGCLSLCLVLALPA.....RVARMPGLERSVRFLPLVH 300

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1634	100.0	300	4	O95407
2	444	27.2	401	4	O00300
3	440.5	27.0	372	4	Q9UHP4
4	425.5	26.0	401	11	O08727
5	424.5	26.0	401	11	O08712
6	395	24.2	302	13	Q9PUS0
7	338.5	20.7	425	4	Q16042
8	333.5	20.4	459	11	Q62327
9	327	20.0	482	11	O88734
10	297	18.2	630	13	Q98SM6
11	291.5	17.8	655	11	Q9EPU5
12	287	17.6	655	4	O75509
13	282.5	17.3	348	12	O57277
14	280.5	17.2	348	12	O57103
15	280.5	17.2	348	12	O57108
16	276	16.9	349	12	O57100
17	274	16.8	349	12	O57291
18	274	16.8	349	12	O57101
19	274	16.8	349	12	O57102

20	273	16.7	349	12	O57099	O57099 monkeypox v
21	265	16.2	350	12	O57116	O57116 cowpox viru
22	264.5	16.2	355	12	O85308	O85308 cowpox viru
23	262.5	16.1	349	12	O57110	O57110 variola vir
24	262.5	16.1	349	12	O57111	O57111 variola vir
25	262.5	16.1	349	12	O89118	O89118 variola vir
26	262.5	16.1	349	12	O89098	O89098 variola vir
27	262	16.0	348	12	O57112	O57112 variola vir
28	262	16.0	348	12	O85407	O85407 variola vir
29	261.5	16.0	349	12	O57284	O57284 camelpox vi
30	261.5	16.0	349	12	O57098	O57098 camelpox vi
31	259.5	15.9	349	12	O57305	O57305 cowpox viru
32	259.5	15.9	360	12	O57118	O57118 cowpox viru
33	258.5	15.8	351	12	O57117	O57117 cowpox viru
34	258.5	15.8	351	12	O73559	O73559 cowpox viru
35	257.5	15.8	326	12	O57120	O57120 cowpox viru
36	257.5	15.8	349	12	O57097	O57097 camelpox vi
37	254.5	15.6	326	12	O57122	O57122 cowpox viru
38	254.5	15.6	349	12	O57109	O57109 variola vir
39	253.5	15.5	347	12	O57115	O57115 cowpox viru
40	251.5	15.4	347	12	O57119	O57119 cowpox viru
41	250.5	15.3	351	12	O57121	O57121 cowpox viru
42	249	15.2	283	6	O9XSZ8	O9XSZ8 cercopithec
43	245.5	15.0	350	12	O57123	O57123 cowpox viru
44	239	14.6	616	4	O9Y606	O9Y606 homo sapien
45	233.5	14.3	625	11	O35305	O35305 mus musculu

ALIGNMENTS

RESULT 1

O95407	ID	O95407	PRELIMINARY;	PRT;	300 AA.
AC	O95407;				
DT	01-MAY-1999	(TrEMBLrel. 10, Created)			
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)			
DT	01-JUN-2001	(TrEMBLrel. 17, Last annotation update)			
DE	DECOY RECEPTOR 3 (M68)	(M68C) (M68C) (DJ583P15.1.1).			
GN	DCR3 OR TR6 OR TNFRSF6B.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99087336;	PubMed=9872321;			
RA	Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,				
RA	Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,				
RA	Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,				
RA	Goddard A.D., Botstein D., Ashkenazi A.;				
RT	"Genomic amplification of a decoy receptor for Fas ligand in lung and				
RT	colon cancer."				
RL	Nature 396:699-703(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BLOOD;				
RX	MEDLINE=99253915;	PubMed=10318773;			
RA	Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;				
RT	"A newly identified member of tumor necrosis factor receptor				
RT	superfamily (TR6) suppresses LIGHT-mediated apoptosis."				
RL	J. Biol. Chem. 274:13733-13736(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PANCREAS;				
RX	MEDLINE=20122600;	PubMed=10655513;			
RA	Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,				
RA	Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.F.;				
RT	"Overexpression of M68/DCR3 in human gastrointestinal tract tumors				
RT	independent of gene amplification and its location in a four-gene				
RT	cluster."				
RL	Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).				
RN	[4]				

```
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104419; AAD03056.1; -
DR EMBL; AF134240; AAD29688.1; -
DR EMBL; AF211796; AAF35244.1; -
DR EMBL; AF211793; AAF33685.1; -
DR EMBL; AF211794; AAF33686.1; -
DR EMBL; AL121845; CAC03668.1; -
DR HSSP; P25942; ICDF.
DR InterPro; IPR000501; EGF-like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 3; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00550; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;

Query Match 100.0%; Score 1634; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 6.4e-139;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 1 MRALEGGSLCLVLPVPAVGVGVAETPTVPRDAETGERLVCAQCPTGVFVOR 60
Db 1 MRALEGGSLCLVLPVPAVGVGVAETPTVPRDAETGERLVCAQCPTGVFVOR 60
QY 61 PCRRDSPTTCGPPRRHYTFQWNYLRCRCVNLGGEREEERACHATHNRCRCRTGFF 120
Db 61 PCRRDSPTTCGPPRRHYTFQWNYLRCRCVNLGGEREEERACHATHNRCRCRTGFF 120
QY 121 AHAGFCLEHASCPPGAGVIAPGTPTSONTCQPCPGTFSASSSSSCQPHRNCRTALGLA 180
Db 121 AHAGFCLEHASCPPGAGVIAPGTPTSONTCQPCPGTFSASSSSSCQPHRNCRTALGLA 180
QY 181 LNVPGSSSHDTCTCTGPPSLRVPGAECERAVIDFVAFQDISIKRLQLLQALEAPE 240
Db 181 LNVPGSSSHDTCTCTGPPSLRVPGAECERAVIDFVAFQDISIKRLQLLQALEAPE 240
QY 241 GWGPTPRAGRAALQLKRLRLTELLGAQDQALLVRLQLARVAMFGLERSVRERLPVLV 300
Db 241 GWGPTPRAGRAALQLKRLRLTELLGAQDQALLVRLQLARVAMFGLERSVRERLPVLV 300

RESULT 2
O00300 PRELIMINARY; PRT; 401 AA.
AC O00300; O60236;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
```

```
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; AB002146; BAA25910.1; -.
DR EMBL; AB008822; BAA32076.1; -.
DR EMBL; AB008821; BAA32076.1; JOINED.
DR HSSP; P25942; ICDF.
DR MIM; 602643; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00550; TNFR_NGFR_2; 2.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 401 OSTEOPROTEGERIN.
FT DOMAIN 23 183 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;

Query Match 27.2%; Score 444; DB 4; Length 401;
```

```

Best Local Similarity 39.6%; Pred. No. 5.6e-32;
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LLCLVLALLPFAVRGVAET--PTYPRDAETGERLVCAQCPTGTFVQRCRRDSPT 68
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 LLCCAL---VFLDISIKWTQTFEPKYLHYDEETSHQLLCKDKCPGTYLKQHCCTAKWKT 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 69 TCGPCPPHYTQFWNYLERCRVNCVLCGRREEARACHATHNRACRCRTGFFAHAGFCLE 128
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 VCAPPDHYTDSWHTSDCLYCSVPCKELQYVQKCNTRHNRVCCKEGRYLEIEFCILK 120
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 129 HASCPPGAGVIAPGTPSQNTQCPQPPGFSASSSSQCOQPHRNCATGALNVPQSSS 188
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 HNSCPGFGVQAGPPTVNCRCRDPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 189 HDTLCTSCGFLPLSTRVPGAE--CERAVIDF 218
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 HDNI---CSGNSSTQKCGIDVTLCCEAFFR 209
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
Q9UHP4 PRELIMINARY; PRT; 372 AA.
AC Q9UHP4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684 (1999).
DR EMBL; AF134187; AAF20168.1; -
DR HSSP; P25942; ICDF.
DR InterPro; IPR000488; Death.
DR ProDom; PF00020; TNFR_c6; 3.
DR SMART; SM00005; TNFR_c6; 1.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT NON_TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 27.0%; Score 440.5; DB 4; Length 372;
Best Local Similarity 41.2%; Pred. No. 1.1e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 34 PTYPWRDAETGERLVCAQCPTGTFVQRCRRDSPTTCGCPPPHYTQFWNYLERCRVNV 93
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 PXYLHYDEETSHQLLCKDKCPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDCLYCS 64
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 94 LCGEREEARACHATHNRACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQCP 153
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 65 VKRELQYVQKCNTRHNRVCCKEGRYLEIEFCILKHSRCPGFGVQAGPPTVNCRCR 124
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 154 PPGTSSASSSSQCOQPHRNCATGALNVPQSSSDHTLCTCTGTPPLSTRVPGAE--C 211
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 125 PDGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSSTQKCGIDVTLC 181
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 212 ERAVIDF 218
   || | | |
Db 182 EEAFFR 188

```

```

RESULT 4
O08727 PRELIMINARY; PRT; 401 AA.
ID O08727;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF).
GN TNFRSF11B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Fan H.-L., Trall G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319 (1997).
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; U94330; AAB53707.1; -
DR HSSP; P25942; ICDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; TNFR_4.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 401 OSTEOPROTEGERIN.
FT DOMAIN 23 201 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 401 AA; 46192 MW; FEC6A3F1D4E573A CRC64;

Query Match 26.0%; Score 425.5; DB 11; Length 401;
Best Local Similarity 39.5%; Pred. No. 2.6e-30;
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;

```

```

QY 34 PTYPWRDAETGERLVCAQCPPTGTFVQPCRRDSTTTCGPPCPRHRYTQFWNYLRCRYCNV 93
DR HSSP; P25942; 1CDF.
DR MGD; MGI:109587; Tnfrsf11b.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001388; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21 OSTEOPROTEGERIN.
FT CHAIN 22 401 4 X TNFR-CYS.
FT DOMAIN 23 201 TNFR-CYS 1.
FT REPEAT 23 63 TNFR-CYS 2.
FT REPEAT 64 106 TNFR-CYS 3.
FT REPEAT 107 143 TNFR-CYS 4.
FT REPEAT 144 201 DEATH DOMAIN.
FT DOMAIN 306 365 BY SIMILARITY.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 R -> P (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 138 138 I -> R (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).
FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 26.0%; Score 424.5; DB 11; Length 401;
Best Local Similarity 39.0%; Pred. No. 3.2e-30;
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;

QY 34 PTYPWRDAETGERLVCAQCPPTGTFVQPCRRDSTTTCGPPCPRHRYTQFWNYLRCRYCNV 93
Db 26 PKYLHYDPETGTHQLLCKCAPGYLKHQCTVRRKTLVCPGDHSTYDTSWHTSDCYVCS 85
QY 94 LCGEREERARACHATHNRACRRTGTFFAHAGFCLEHASCPGAGVIAPGTPSNTQCPC 153
Db 86 VKCLETVQKECNTRNVRVCEEGRYLEFELCKLHRSCPPGLGVLAQGPPTVCKRC 145
QY 154 PCGTFSASSSSQCPHRCNTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGAEE--C 211
Db 146 PDGFFSGETSSKAPCKHNTCSGLILLIOKGNATHDNV---CSGNREATQNGIDVTLC 202
QY 212 ERAVIDFAFQDISIKRLQRLQAL 236
Db 203 EEAFFFAVPTKIIPNWLVLVDLSL 227

RESULT 6
QYPU50 PRELIMINARY; PRT; 302 AA.
ID QYPU50
AC QYPU50
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

```

DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00500; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER
SQ SEQUENCE 425 AA; 44608 MW; 1B24A97E3AD4CF9F CRC64;

Query Match 20.7%; Score 338.5; DB 4; Length 425;
Best Local Similarity 30.1%; Pred. No. 1.8e-22;
Matches 82; Conservative 43; Mismatches 110; Indels 37; Gaps

QY 46 RLVCACCPGCTFFVORCRDSDPTTCGCPRRHHYTOFWNVYLERCRYCNVLCGEBEERAC 105
DB 15 QMCCSKCSPGQAHKVFCTKTSDFVDCSEDESTVTLQNMVPECLSCGRCSSDQVETQAC 74
QY 106 HATHNRACRGTGFFAHAG-----FCLHASCPPGAGVIAPGTPSQNTQCQCPGPGTES 159
DB 75 TRQNRICTRPGWYCALSKQECRCALPLKCRPGFGVARGTETSDVVKPCAPGTES 134
QY 160 ASSSSSEQPHRNCTALGIALNVPSSSHDTLCTSGTGPLSTRVPGAECERAVIDFV 219
DB 135 NTTSSDICTRPHQICNVVA---IPGNASMDAVCTSTS---PTRSMAPGAVHLPPQV--- 184
QY 220 AFODISIKRLQRLQLEAPE-----GWGPTPRA-----GRAALQLKRLRLLFELLAGQDG 270
DB 185 ---STRSQHTQPTPEPSTAPSTFLLPMGFPSPPAEGSTGDFALPVLGVGTAL-----G 236
QY 271 ALLVRLQLAAL--RVARMPP--GLERSVRERFLP 298
DB 237 LLIIGVNVCVIMTQVKKKPLCLQREAKRVPHLP 268

RESULT 8
Q62327 PRELIMINARY; PRT; 459 AA.

AC Q62327;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]
RN R1 SEQUENCE FROM N.A.
RC STRAIN=MOD;
RX MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
gene."
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAAS3981.1; -.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
FT NON_TER 1
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 20.4%; Score 333.5; DB 11; Length 459;
Best Local Similarity 29.7%; Pred. No. 5.3e-22;
Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps

```
QY 46 RLVAACPPGTFVQRCRRDPTTCGCPRRHYTQFWNYLRCRYCNVLCGEREEARAC 105
DB 37 QMCCARCPGQYVYKHCNKTSDTVACDCEASMYTQVWQFRTCLSCSSCSSTDQVETRAC 96
QY 106 HATHNACRCRTGFF---AHAGF---CLEHASCPPGAGVIAPGTPSNTQCPGPGTF 158
DB 97 TKOONRVACACEAGRYCALKTHSGSCRCQMLRSKCGFGVASSRAPNGVNLKACAPGTF 156
QY 159 SASSSECOQPHRNCNTALGLNVPGSSSHDTLCT---SCTGFFPLSTRVPGAEBCERA 214
DB 157 SDTSTSDVCRPHRCSILA---IFGNASTDAVCAPESTLSAIPRTLIVSQPEPTRSQ 212
QY 215 VIDFAQDISIKRLQRLQALQEAPEGWGTP-----RAGRAALQKLRRRLTELGAQD 269
DB 213 PLD-----QEPGSPQTSILTSL-----GSTPIEQSTKGISLPIGLVGTSL----- 257
QY 270 GALLVRLQALQ-----RVARMPLGERSVRERFLP 298
DB 258 GLMLGLVNCFILVQRKKPSCLOQDAKVPHPV 290

RESULT 9
ID O88734 PRELIMINARY; PRT; 482 AA.
AC O88734;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE P80 TNF-ALPHA RECEPTOR.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hurlie B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor Gene: Genomic Structure and
RL Characterization of the two Transcripts.";
RL Genomics 0:0-0(0).
DR EMBL; Y14619; CAAT4969.1; JOINED.
DR EMBL; Y14620; CAAT4969.1; JOINED.
DR EMBL; Y14621; CAAT4969.1; JOINED.
DR EMBL; Y14622; CAAT4969.1; JOINED.
DR EMBL; Y14623; CAAT4969.1; JOINED.
DR EMBL; Y14679; CAAT4969.1; JOINED.
DR HSSP; P19438; 1NCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 3.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 20.0%; Score 327; DB 11; Length 482;
Best Local Similarity 29.3%; Pred. No. 2.1e-21;
Matches 82; Conservative 43; Mismatches 109; Indels 46; Gaps 10;

QY 46 RLVAACPPGTFVQRCRR-----DSPTTCGCPRRHYTQFWNYLRCRYCNVLCGER 98
DB 52 QMCCARCPGQYVYKHCNKTSDTVACDCEASMYTQVWQFRTCLSCSSCSSTDQVETRAC 111
QY 99 EEEARACHATHNACRCRTGFF---AHAGF---CLEHASCPPGAGVIAPGTPSNTQCOQ 151
DB 112 QVETRACHTQQNRVACACEAGRYCALKTHSGSCRCQMLRSKCGFGVASSRAPNGVNLCK 171
QY 152 PCPPPTSSSSSSSECOQPHRNCNTALGLNVPGSSSHDTLCT-----SCTGFFPLSTRVPG 207
DB 172 ACAPGTFSDTSTSDVCRPHRCSILA---IPGNASTDAVCAPESTLSAIPRTLIVYSQ 227
QY 208 AEECERAVIDFVAFQDISIKRLQRLQALQEAPEGWGTP-----RAGRAALQKLRRRLT 262
```

```
DB 228 PEPTRSQPLD---QEPGSPQTSILTSL-----GSTPIEQSTKGISLPIGLVGT 277
QY 263 ELLGAQDGGALLVRLQALQ-----RVARMPLGERSVRERFLP 298
DB 278 SL-----GLMLGLVNCFILVQRKKPSCLOQDAKVPHPV 312

RESULT 10
ID Q98SM6 PRELIMINARY; PRT; 630 AA.
AC Q98SM6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DEATH RECEPTOR 6 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349908; AAK29666.1; -.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 630 AA; 68977 MW; 53C53BD1C4B25567 CRC64;

Query Match 18.2%; Score 297; DB 13; Length 630;
Best Local Similarity 34.2%; Pred. No. 1.4e-18;
Matches 55; Conservative 27; Mismatches 79; Indels 0; Gaps 0;

QY 40 DAETGRLVCAACPPGTFVQRCRRDPTTCGCPRRHYTQFWNYLRCRYCNVLCGER 99
DB 22 DRATNOELICDKCPAGTYVSKHCTKSTLRCSPPGDTFTKHENGIERCHPCRKPCPLM 81
QY 100 EEARACHATHNACRCRTGFFAHAGFCLHASCPPGAGVIAPGTPSNTQCOQCPGTF 159
DB 82 IERTHTALTDRCTCLSGTFQINDTCVPTVCPGWSGVRKGTETEDVRCKPCPRGTF 141
QY 160 ASSSSECOQPHRNCNTALGLNVPGSSSHDTLCTCTCTGFP 200
DB 142 DVPSSVMKCKTYTDCFGKNNVVVKPGTKESDNVCGSPASLP 182

RESULT 11
ID Q9EPU5 PRELIMINARY; PRT; 655 AA.
AC Q9EPU5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=KIDNEY;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
(RD6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF322069; AAG38115.1; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
```

```

DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
DR SEQUENCE 655 AA; 71909 MW; 1A97C1432799E4FB CRC64;

Query Match 17.8%; Score 291.5; DB 11; Length 655;
Best Local Similarity 28.6%; Pred. No. 4.5e-18;
Matches 73; Conservative 37; Mismatches 130; Indels 15; Gaps

Qy 12 LCLVLALPALLPVAVRGVAAETTYPRDAETGERLVCAQCPCPGTVQVQRDRSDPTTCG 71
Db 30 LLLGLFSLTIAAQPEQKTLSLPGTYRHVDRTQGVITCDKCPAGTVVSEHTNMSLRVCS 89
Qy 72 PCPPRHYYTFQWNTLERCYKNCVLGCGREERAEARACHATHNRACRCRTGFFAHAGFCLEHAS 131
Db 90 SCPAGITFRHENGIERCHDCSCQPWPMTIERLPCAALTDEICCPGMYQSNGTCAPIHV 149
Qy 132 CPPGAGVIAGTFSQNTQCPQPPGTFSSASSSSSQCOQPHRNCNTALGLALNVPGSSSHT 191
Db 150 CPVGGWVRKKGTEDEYRCKQCARGTFSDPVSSVMKCKAHTDCLGQNLVWPKGTKETDN 209
Qy 192 LCTSCCTCFPL--STRVPGAEECEARAVIDPFAQDISIKRLQRLQLQAEPGWGTPRA 248
Db 210 VC----CMRLFFSTNPPSGTVTFSHPEHMEASHDVPSSITYE-----PGQMNSTDN 257
Qy 249 GRAALQKLRRRLUTE 263
Db 258 STASVRTKVPESGIEE 272

```

```

RESULT 12
O75509 PRELIMINARY; PRT; 655 AA.
ID O75509;
AC O75509;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE . TNFR-RELATED DEATH RECEPTOR-6 (DJ181J13.1) (DR6 (TNFR-RELATED DEATH
DE RECEPTOR-6)).
GN DR6 OR DJ181J13.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G.,
RA Vincenz C., Aggarwal B.B., Dixit V.M.;
RT "Identification and functional characterization of DR6, a novel death
RT domain-containing TNF receptor.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Parker A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF068868; AAC34583.1; -.
DR EMBL; AL096801; CAB75692.1; -.
DR HSSP; P07174; INGR.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.

```

KW Receptor.
SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 17.6% Score 287; DB 4; Length 655;
Best Local Similarity 34.3%; Pred. No. 1.1e-17;
Matches 58; Conservative 23; Mismatches 88; Indels 0; Gaps 0;

Qy 35 TYPRDAETGERLVCAQCPCPGTFVQRPCRDRDPTTCGCPPHRYTQFWNYLERCRYCNVL 94
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 53 TYRHVDRTAGQLTCDKCPACTYVSEHCTNTSLRVSSCPVGTTRHENGEIKCHDCSQP 112
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 95 CGEREERARACHATHNRCACRORTGFHAHGCLDEHASCPPGAGVIAPGTPSQNTQCQPCP 154
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 113 CPWMIEKLPCAALTDRRECTCPGFMFOSNATCAPHTVCVPVGVRKKGTETEDVRCKQA 172
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 155 PGTFSSASSSSEQCPHRNCTALGLANVPQGSSSHDTLCTSCFTGPPLST 203
|||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 173 RGTFSDFSPVMNKCKAYTDCLSQLNLVVKPGTKETDNVCGTLPSFSST 221
|||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 13
O57277 PRELIMINARY; PRT; 348 AA.

ID AC O57277
AC O57277;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OX Orthopoxvirus.
NCBI_TaxID=10244;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1996(96-17), ZAIRE-1996 (96-16);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U8543; AAB94378.1; -
DR EMBL; U87841; AAB94358.1; -
DR HESP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGRF_1; 2.
DR PROSITE; PS00050; TNFR_NGRF_2; 2.
SQ SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;

Query Match 17.3% Score 282.5; DB 12; Length 348;
Best Local Similarity 30.9%; Pred. No. 1.5e-17;
Matches 64; Conservative 33; Mismatches 97; Indels 13; Gaps 3;

Qy 9 LSLCLVLALLPALFPVAVRGVAETPTYPRWDAETGERLVCAQCPCPGTFVQRCDRSPT 68
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 10 LFLSCIIRGLDLAPHASNGCKRDNEYRSN-----LCCLSCPCTGYASRLCDSKTNT 63
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 69 TCGPCPPRHYYTQFWNYLERCRYCNVLGEREEERACHATHNRCACRTGFF-----AH 122
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 64 QCTPCGSTFTSHNNHLQAQLCSNGCRDSNOVETRSCNTTHNRICECSPGYCYLLKGSSG 123
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 123 AGFCLEHASCPPGAGVTAPGTPSQNTQCQPCPGTFSSASSSSBOCOPHRNCTALGLANL 182
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 124 CRTCIKTCKIGYGV-SGYITSGDVICSPCGPGTYSHITSVSDTKCEPVTSNTFNIDVE 182
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 183 VPGSSSHDTLCTSCFTGPPLSTRVPFAE 209
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 183 INLPVNDTSCRITTTGLSESISTSE 209

RESULT 14

```
O57103
ID O57103 PRELIMINARY; PRT; 348 AA.
AC O57103;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1979 (79-0005);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87847; AB94364.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;

Query Match 17.2%; Score 280.5; DB 12; Length 348;
Best Local Similarity 30.4%; Pred. No. 2.3e-17;
Matches 63; Conservative 34; Mismatches 97; Indels 13; Gaps 3;

QY 9 LSLLLCLVLPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPGTFVQRPCCRDSPT 68
DB 10 LFLSCLIIINGRDIAHPNSGKCKDNEYRSN-----LCCLSCPPTVASRLCDSKNT 63
QY 69 TCGPCPPRHYTOFWNYLRCRYCNVLCGEREEARACHATHNRACRGTGFF-----AH 122
DB 64 OCTPCGSDTFTSHNNHQAQLSCNGRCDNSQVETRSCNTTHNRICECSPGYICLLKSSG 123
QY 123 AGFCLEHASCPPGAGVIAFGTFSQNTQCPGPTFSASSSSSEOCQPHRNCALGLALN 182
DB 124 CRTICSKTKCGIGYGV-SGYTSTGDIVCSGPCGPGTYSHTVSSDCKEPTVTSNTFNVIDVE 182
QY 183 VPGSSSHDTLCTSGTGFPLSTRVPGAE 209
DB 183 INLYPVNDTSCRTTTTGLSESISTSE 209

Search completed: May 10, 2002, 10:59:02
Job time: 356 sec
```

```
O57108
ID O57108 PRELIMINARY; PRT; 348 AA.
AC O57108;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1970 (CONGO-8);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AB94367.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.

Query Match 17.2%; Score 280.5; DB 12; Length 348;
Best Local Similarity 30.4%; Pred. No. 2.3e-17;
Matches 63; Conservative 34; Mismatches 97; Indels 13; Gaps 3;

QY 9 LSLLLCLVLPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPGTFVQRPCCRDSPT 68
DB 10 LFLSCLIIINGRDIAHPNSGKCKDNEYRSN-----LCCLSCPPTVASRLCDSKNT 63
QY 69 TCGPCPPRHYTOFWNYLRCRYCNVLCGEREEARACHATHNRACRGTGFF-----AH 122
DB 64 OCTPCGSDTFTSHNNHQAQLSCNGRCDNSQVETRSCNTTHNRICECSPGYICLLKSSG 123
QY 123 AGFCLEHASCPPGAGVIAFGTFSQNTQCPGPTFSASSSSSEOCQPHRNCALGLALN 182
DB 124 CRTICSKTKCGIGYGV-SGYTSTGDIVCSGPCGPGTYSHTVSSDCKEPTVTSNTFNVIDVE 182
QY 183 VPGSSSHDTLCTSGTGFPLSTRVPGAE 209
DB 183 INLYPVNDTSCRTTTTGLSESISTSE 209

RESULT 15
O57108
ID O57108 PRELIMINARY; PRT; 348 AA.
AC O57108;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1970 (CONGO-8);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AB94367.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:53:51 ; Search time 15.03 Seconds
(without alignments)
731.833 Million cell updates/sec

Title: US-09-280-567-2
Perfect score: 1634
Sequence: 1 MRALEGPLSLGLVLPALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	353.5	21.6	461	1 TNR2_HUMAN	P20333 homo sapien
2	332.5	20.3	474	1 TNR2_MOUSE	P32119 mus musculu
3	315	19.3	435	1 TNR2_HUMAN	P36941 homo sapien
4	277	17.0	415	1 TNR2_MOUSE	P50284 mus musculu
5	262.5	16.1	349	1 VC22_VARV	P34015 variola vir
6	246	15.1	283	1 TR14_HUMAN	Q92956 homo sapien
7	236.5	14.5	325	1 VT2_SFVKA	P25943 shope fibro
8	226	13.8	277	1 OX40_HUMAN	P43489 homo sapien
9	215	13.2	326	1 VT2_MXVL	P29825 myxoma viru
10	214	13.1	271	1 OX40_RAT	P15725 rattus norv
11	211	12.9	277	1 CD40_HUMAN	P25942 homo sapien
12	203	12.4	289	1 CD40_MOUSE	P27512 mus musculu
13	202	12.4	269	1 CD40_BOVIN	Q28203 bos taurus
14	198.5	12.1	272	1 OX40_MOUSE	P47741 mus musculu
15	186.5	11.4	595	1 CD30_HUMAN	P28908 homo sapien
16	185	11.3	256	1 41BB_MOUSE	P20334 homo sapien
17	176	10.8	416	1 NGFR_CHICK	P18519 gallus gall
18	175.5	10.7	427	1 NGFR_HUMAN	P08138 homo sapien
19	174	10.6	255	1 41BB_HUMAN	Q07011 homo sapien
20	170	10.4	425	1 NGFR_RAT	P07174 rattus norv
21	163	10.0	332	1 FASA_PIG	O77736 sus scrofa
22	160.5	9.8	471	1 TNR1_BOVIN	O19131 bos taurus
23	155.5	9.5	260	1 CD27_HUMAN	P26842 homo sapien
24	155.5	9.5	327	1 FASA_MOUSE	P25446 mus musculu
25	155	9.5	323	1 FASA_BOVIN	P51867 bos taurus
26	153	9.4	241	1 TR18_HUMAN	Q9Y5u5 homo sapien
27	148	9.1	250	1 CD27_MOUSE	P41272 mus musculu
28	147.5	9.0	5376	1 ZAN_MOUSE	O88799 mus musculu
29	145	8.9	335	1 FASA_HUMAN	P25445 homo sapien
30	144	8.8	324	1 FASA_RAT	Q63199 rattus norv
31	137.5	8.4	454	1 TNR1_MOUSE	P25118 mus musculu
32	129.5	7.9	1877	1 PK5_MOUSE	Q04592 mus musculu
33	128.5	7.9	417	1 WSL1_HUMAN	Q93038 h wsl-1 pro

34	128.5	7.9	3635	1 LMA5_MOUSE	Q61001 mus musculu
35	127	7.8	1192	1 LMG2_MOUSE	Q61092 mus musculu
36	125.5	7.7	461	1 TNR1_RAT	P22934 rattus norv
37	125.5	7.7	1255	1 ERB2_HUMAN	P04626 homo sapien
38	124.5	7.6	1696	1 PK5_BRACL	Q9nj15 branchiosto
39	124.5	7.6	1713	1 LMA3_HUMAN	Q16787 homo sapien
40	124.5	7.6	3106	1 LMA2_MOUSE	Q60675 mus musculu
41	123.5	7.6	455	1 TNR1_HUMAN	P19438 homo sapien
42	123.5	7.6	2813	1 VWF_CANFA	Q28295 canis famil
43	123	7.5	2569	1 LMA3_MOUSE	Q61789 mus musculu
44	120	7.3	1609	1 LMG1_HUMAN	P11047 homo sapien
45	120	7.3	2318	1 NTC3_MOUSE	Q61982 mus musculu

ALIGNMENTS

RESULT	1
TNR2_HUMAN	
ID	TNR2_HUMAN
AC	P20333; STANDARD; PRT; 461 AA.
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBP2) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
GN	TNFRSF1B OR TNFR2 OR TNFR.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=90260639; PubMed=2160731;
RA	Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA	Dower S.K., Cosman D., Goodwin R.G.;
RT	"A receptor for tumor necrosis factor defines an unusual family of
RT	cellular and viral proteins.";
RL	Science 248:1019-1023(1990).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91045991; PubMed=2172983;
RA	Kohn T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA	Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT	"A second tumor necrosis factor receptor gene product can shed a
RT	naturally occurring tumor necrosis factor inhibitor.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96299745; PubMed=8661109;
RA	Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA	Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA	Brodeur G.M.;
RT	"Physical mapping and genomic structure of the human TNFR2 gene.";
RL	Genomics 35:94-100(1996).
RN	[4]
RP	SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX	MEDLINE=90349572; PubMed=2166946;
RA	Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA	Ringold G.M.;
RT	"Complementary DNA cloning of a receptor for tumor necrosis factor
RT	and demonstration of a shed form of the receptor.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN	[5]
RP	SEQUENCE OF 27-31.
RX	MEDLINE=90110215; PubMed=2153136;
RA	Engelmann H., Novick D., Wallach D.;
RT	"Two tumor necrosis factor-binding proteins purified from human
RT	urine. Evidence for immunological cross-reactivity with cell surface
RT	tumor necrosis factor receptors.";
RL	J. Biol. Chem. 265:1531-1536(1990).
RN	[6]
RP	SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.

RX MEDLINE=91056048; PubMed=2173696;
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.;
 RT "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RP [7]
 RN CHARACTERIZATION.
 RX MEDLINE=93016040; PubMed=1328224;
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.
 RX MEDLINE=99221490; PubMed=10206649;
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
 RT "Structural basis for self-association and receptor recognition of
 RT human TRAF2.";
 RL Nature 398:533-538(1999).
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 CC LEVEL ON THREONINE RESIDUES.
 CC -!- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND
 CC WYETH-AYERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
 CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -!- DATABASE: NAME-PROW: NOTE-CD guide CD120b entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".
 CC -!- DATABASE: NAME-Enbrel; NOTE-Clinical information on Enbrel;
 CC WWW="http://www.enbrelinfo.com/".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M32315; AAC59929.1; -;
 DR EMBL; M35057; AAC63262.1; -;
 DR EMBL; U52165; AAC50622.1; -;
 DR EMBL; U52156; AAC50622.1; JOINED.
 DR EMBL; U52157; AAC50622.1; JOINED.
 DR EMBL; U52158; AAC50622.1; JOINED.
 DR EMBL; U52159; AAC50622.1; JOINED.
 DR EMBL; U52160; AAC50622.1; JOINED.
 DR EMBL; U52161; AAC50622.1; JOINED.
 DR EMBL; U52162; AAC50622.1; JOINED.
 DR EMBL; U52163; AAC50622.1; JOINED.
 DR EMBL; U52164; AAC50622.1; JOINED.
 DR EMBL; M55994; AAC36755.1; -;
 DR PIR; A35356; A35356.
 DR PIR; A36007; A36007.
 DR PIR; A36475; A36475.
 DR PIR; B35010; B35010.
 DR PIR; A23666; A23666.
 DR PDB; 1CA9; 12-APR-99.
 DR MIM; 191191; -;
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.
 *W Receptor; Transmembrane; Glycoprotein; Repeat; Signal;

KW Phosphorylation; Pharmaceutical; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 258 287 POTENTIAL.
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 201 4 X TNFR-CYS.
 FT REPEAT 39 76 TNFR-CYS 1.
 FT REPEAT 77 118 TNFR-CYS 2.
 FT REPEAT 119 162 TNFR-CYS 3.
 FT REPEAT 163 201 TNFR-CYS 4.
 FT DISULFID 40 53 BY SIMILARITY.
 FT DISULFID 54 67 BY SIMILARITY.
 FT DISULFID 57 75 BY SIMILARITY.
 FT DISULFID 78 93 BY SIMILARITY.
 FT DISULFID 96 110 BY SIMILARITY.
 FT DISULFID 100 118 BY SIMILARITY.
 FT DISULFID 120 126 BY SIMILARITY.
 FT DISULFID 134 143 BY SIMILARITY.
 FT DISULFID 137 161 BY SIMILARITY.
 FT DISULFID 164 179 BY SIMILARITY.
 FT CARBOHYD 171 171 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 141 141 R -> P (IN REF. 4).
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).
 FT CONFLICT 363 363 A -> T (IN REF. 4).
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

 Query Match 21.6%; Score 353.5; DB 1; Length 461;
 Best Local Similarity 29.8%; Pred. No. 1.1e-20;
 Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;

 QY 8 GLSLCLVLALPALLPVPVAVRGVAETPTYPWRDAEAGE-----RLVCAQCPCPG 55
 DB 13 GLELWAAHALPA-----QVAFTPYAP----EPGTCRLREYDYDTAQMCCSKCSPG 60

 QY 56 TFVQRCRRDSPTTCPCPPRHVYTFQWNYLCRCYCNVLCGEREEARACHATHNACRC 115
 DB 61 QHAKVCTKTSVDCSCDSYITQLWNVPECLSCGRCSSDQVETQACTRQNRICTC 120

 QY 116 RTGFFAHAG-----FCLHASCPPGAGVIAPTQPCPPGTPGTSASSSSSEQC 169
 DB 121 RFGWCALSKQEGCRICAPLRCRPGFVGARPGTETSDVVKPCAPGTFSTSTSDICR 180

 QY 170 PHRNCTALGALNVPSSSHSDTLCTSGTGFPLSTRYPGAECECERAVIDFVAFQDISIKRL 229
 DB 181 PHQICNVVA-----IPGNASRDVAVCTSTS---PTRSMAPGAVHLPQPV-----STRSQHT 227

 QY 230 QRLQLALEAPE-----GWGPTPRA-----GRAALQLKRLRRLTELLGAQDQALVRLQAL 280
 DB 228 QTPPEPSTAPSTSFLLPMGFPSPGAEGSTGDFALPGLVGVVTL-----GLLIIGVNVCV 282

 QY 281 ----RVARMP-GLERSVRRFLP 298
 DB 283 IMTVKKKKPLCLQREAKVPHP 304

 RESULT 2
 TNFR2_MOUSE
 ID TNFR2_MOUSE STANDARD; PRT; 474 AA.
 AC P25119; P97893;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
 GN TNFRSF1B OR TNFR2 OR TNFR-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE-91187885; PubMed=1849278;
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.;
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific.";
 RL proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE OF 1-26 FROM N.A.
 RC STRAIN-NOD;
 RA Jacob C.O., Liu J.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-22 FROM N.A.
 RC TISSUE=Liver;
 RA Kissnerghis M., Fellows R., Feldmann M., Chernajovsky Y.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
 CC -!- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M60469; AAA39752.1; -;
 DR EMBL; M59378; AAA40463.1; -;
 DR EMBL; U39488; AAA85021.1; -;
 DR EMBL; X87128; CAA60618.1; -;
 DR PIR; B38634; B38634.
 DR HSSP; P19438; INCF.
 DR MGD; MGI:1314883; Tnfrsf1b.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 4.
 DR ProDom; PD000771; TNFR_C6; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00650; TNFR_NGFR_2; 3.
 DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 259 288 POTENTIAL.
 FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 203 4 X TNFR-CYS.
 FT REPEAT 39 77 TNFR-CYS 1.
 FT REPEAT 78 119 TNFR-CYS 2.
 FT REPEAT 120 164 TNFR-CYS 3.
 FT REPEAT 165 203 TNFR-CYS 4.
 FT DISULFID 40 54 BY SIMILARITY.
 FT DISULFID 55 68 BY SIMILARITY.
 FT DISULFID 58 76 BY SIMILARITY.
 FT DISULFID 79 94 BY SIMILARITY.
 FT DISULFID 97 111 BY SIMILARITY.
 FT DISULFID 101 119 BY SIMILARITY.
 FT DISULFID 121 127 BY SIMILARITY.
 FT DISULFID 136 145 BY SIMILARITY.
 FT DISULFID 139 163 BY SIMILARITY.
 FT DISULFID 166 181 BY SIMILARITY.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;
 Query Match 20.3%; Score 332.5; DB 1; Length 474;
 Best Local Similarity 29.7%; Pred. No. 4.8e-19;
 Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;
 QY 46 RLVCACQCPGTFVQPRCRDSTTCGCPRRHYTQWNYLRCRYCNVLCGEREEARAC 105
 DB 52 QMCCAKCPGQYVYKHFCNKTSITVCADEASMYTQVWVNFRTCLSCSSCTTDOVEIRAC 111
 QY 106 HATHRACRCRTGFF-----AHAGF---CLEHACPPGAGVIAPGTPSQTQCPQPGTF 158
 DB 112 TQQRNVKACAGRYCALKTHSGRCQRLSKCGPGFVGVSRRAPNGNVLCACAPGTF 171
 QY 159 SASSSSEOCQPHRNCNTALGLALNVPGSSSHDTLCT-----SCTGFPLTRVPAGEECERA 214
 DB 172 SDTSTSDVCRPHRCSILA----IPGNASTDAVCAPESTLSAIPRTLYVSOPEPTRSQ 227
 QY 215 VIDFVAFQDISIKRLQRLQALEAPGEGWTP-----RAGRAALQKLRRRLTELLGAQD 269
 DB 228 PLD---QEPGPGSQTSLTSL-----GSTPIEQSTKGISLPIGLIVGVTSL----- 272
 QY 270 GALLVRLQAL----RVARMPGLERSVRERFLP 298
 DB 273 GLMLGLVNCIILVORRKKPKSLQDRDAKVPHP 305
 RESULT 3
 TNRC_HUMAN
 ID TNRC_HUMAN STANDARD; PRT; 435 AA.
 AC P36941;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
 DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
 GN LTBR OR TNFR OR TNFRSF3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-93252381; PubMed=8486360;
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
 RT "Construction and evaluation of a hncDNA library of human 12p
 RT transcribed sequences derived from a somatic cell hybrid.";
 RL Genomics 16:214-218(1993).
 RN [2]
 RP FUNCTION.
 RX MEDLINE-94225209; PubMed=8171323;
 RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
 RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
 RT "A lymphotoxin-beta-specific receptor.";
 RL Science 264:707-710(1994).
 CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 CC IMMUNE DEVELOPMENT.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L04270; AAA36757.1; -;
 DR HSSP; P25942; LCDF.
 DR MIM; 600979; -.

```
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00505; TNFR_NGFR_2; 3.
DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
KW SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 31 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT DOMAIN 42 211
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
SQ SEQUENCE 435 AA; 46709 MW; 62462856022F656F CRC64;

Query Match 19.3%; Score 315; DB 1; Length 435;
Best Local Similarity 31.8%; Pred. No. 1e-17;
Matches 89; Conservative 29; Mismatches 120; Indels 42; Gaps 12;

QY 3 ALEGGSLLLVLPALLPVAVRGVAETPT-----PWRDA-----ETGERLVCAQC 52
Db 6 ATSAPGLAWPLVLGLFLAASQPAV---PPYASENQTRDQKEYEYEPQHRICCSRC 62
QY 53 PPGTFVQRCRDSPTGCPGPRHYTFQFNVL---EERCYNVLCGEREEARACHATH 109
Db 63 PPGTFVSAKSRIDTVCAATCAENSYNEHNYLTICQLCRPCDPVNG---LEETAPCTSKR 120
QY 110 NRACRCRTGFFAHAGFLE--H-----ASCPPGA-GVIAPGTPSQNTQCQPPGTFSSAS 162
Db 121 KTCRCQCPMFC-AAWALECTHCELLSDCPGCTEAEELKDEVCKGNHCVCKAGHFQNTS 179
QY 163 SSSEOCQPHRNCTALGLALNVPGSSHDLTCTSCGTFPLSTRVPGAECECAVIDFVAFQ 222
Db 180 SPSARCQPHTRCENQGLVEAPGTAQSDTCKNPLE-PLPPEMSGTMLMLAVLLPLAFL 238
QY 223 DIS-----IKRLQLQALEAPEGWTTPRAG 249
Db 239 LLATVFVSCIWKSHPSLCRLKGLSLK---RRPQEGPNPVAG 276

RESULT 4
TNRC_MOUSE
ID TNRC_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LTBR OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RZ SEQUENCE FROM N.A.
RC STRAIN-CVB; TISSUE=Lung;

RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression.";
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping.";
RL Genomics 30:312-319(1995).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U29173; AAA68964.1; -
DR EMBL: L38423; AAB00846.1; -
DR EMBL: U30798; AAB81334.1; -
DR HSSP: P25942; ICDF.
DR MGD; MGI:104875; Ltbr.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00505; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 224 244
FT DOMAIN 245 415
FT DOMAIN 42 213
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 40 40
FT CARBOHYD 179 179
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 17.0%; Score 277; DB 1; Length 415;
Best Local Similarity 31.2%; Pred. No. 9.2e-15;
Matches 88; Conservative 29; Mismatches 105; Indels 60; Gaps 14;

QY 6 GP---GLSLGLVLPALLPVAVRGVAETPTPWRDAETGERL---VCAOCPGCTFVQ 59
Db 15 GLLGLLSGL-LVASQPLVPPYRI---ENOTCWDQDREYEPHMDVCCSPGGEFV 69
QY 60 RPCRDSPTTCGCPPRHYTFQFNVL---EERCYNVLCGEREEARACHATHNRCRCR 116
```

```
Db 70 AVCSRSQDVTCKTCPCNSNEHNNHLSLTCOLCRPCDIVLG--FEVAPCTSDRKAECRCQ 127
QY 117 TGFFAHAGFLC-----EHASCPGAGVIA-PGTPSQNT-----OCQPCPPGCTFSASSS 163
Db 128 PGM-----SCVLDNECVICEERLVLCQPGTEAEVTDIMDTDNCVCKFGHFQNTSS 182
QY 164 SSEQCOPHNCRTALGIALNVPSSSHDTICTCTGTPPLSTRVPGAECEERAVIDFAV-- 221
Db 183 PRACQPHTRCEIQGLVEAPGTSYSDTICK-----NPPPEGAMLLAILLSLVLFLL 235
QY 222 -----QDISIKRLQRLQALAEPEGWG-----PTPRA 248
Db 236 FTTVLACAMWRHPSLCRKLGLTLK--RHPEGESPPCPAPRA 275

RESULT 5
ID VC22_VARV STANDARD; PRT; 349 AA.
AC P34015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROTEIN C22/B28 HOMOLOG.
GN GAR.
OS Variola virus.
OC Viruses; GSDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-INDIA-1967 / ISOLATE IND3;
RX MEDLINE-9320281; PubMed-8394129;
RA Shchelkunov S.N., Bilnov V.M., Sandakchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
CC -!- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch.)
CC
CC EMBL; X69198; CAA49137.1; -
CC EMBL; X67117; CAA47540.1; -
CC PIR; D36858; D36858.
CC PIR; S35987; S35987.
CC PIR; S46888; S46888.
CC HSSP; P19438; INCF.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 2
CC ProDom; PD000771; TNFR_c6; 1.
CC SMART; SM00208; TNFR; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Repeat.
KW DOMAIN
FT DOMAIN 31 108 2 X TNFR-CYS.
FT REPEAT 31 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
SQ SEQUENCE 349 AA; 38189 MW; D45D40B5C6E780EF CRC64;

Query Match 16.1%; Score 262.5; DB 1; Length 349;
Best Local Similarity 30.0%; Pred. No. 1.le-13;
Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;
QY 9 LSLCLVLALPALLPVPVAVGVAEPTTPWRDAETGERLVCAOCPPCTFFVQRCRDSPT 68
Db 10 LFLUSCIINGRDAAPTTPPGKCKDTEY-----KRHNLCCLSCPPGTYASRLCDKNT 63
```

```
QY 69 TCGCPPRHYTOFWNYLERYCYNVLGGEREERARACHATHNRACRGTGFF-----AH 122
Db 64 QCTPGSGTFTSRNNHLPACLSGCRGNSNQVETRSNCTTHNRICECSPGYCLLKSSG 123
QY 123 AGCLEHASCPPAGVIAPGTPTSQNTQCQCPGPTFSASSSSSEOCOPHNCRTALGIALN 182
Db 124 CKAVSQTKGIGYGV-SGHTSVGDVICSPCGFGTSHTVSSADKCEPVPNNTFNYIDVE 182
QY 183 VPGSSSHDTLCTCTGTPPLSTRVPGAE 209
Db 183 ITLYPVNDTSCRTTTTGLSESLTSE 209

RESULT 6
ID TRI4_HUMAN STANDARD; PRT; 283 AA.
AC Q92956; Q9UM65;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14 PRECURSOR
DE (HERPESVIRUS ENTRY MEDIATOR) (TUMOR NECROSIS FACTOR RECEPTOR-LIKE 2)
DE (TR2).
GN TNFRSF14 OR HVEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix adenocarcinoma;
RX MEDLINE-97053782; PubMed-8898196;
RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT the TNF/NGF receptor family.";
RL Cell 87:427-436(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97306336; PubMed-9162061;
RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA Porter T.G., Truneh A., Young P.R.;
RT "A newly identified member of the tumor necrosis factor receptor
RT superfamily with a wide tissue distribution and involvement in
RT lymphocyte activation.";
RL J. Biol. Chem. 272:14272-14276(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Cao X.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR TNFSF14. INVOLVED IN LYMPHOCYTE ACTIVATION.
CC PLAYS AN IMPORTANT ROLE IN HSV PATHOGENESIS BECAUSE IT ENHANCED
CC THE ENTRY OF SEVERAL WILDTYPE HSV STRAINS OF BOTH SEROTYPES INTO
CC CHO CELLS, AND MEDIATED HSV ENTRY INTO ACTIVATED HUMAN T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC IN LUNG, SPLEEN, AND THYMUS.
CC -!- SIMILARITY: CONTAINS 1 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch.)
CC
CC EMBL; U70321; AAB58354.1; -
CC EMBL; U81232; AAD00505.1; -
CC EMBL; AF153578; AAF75588.1; -
CC HSSP; P25942; ICDF.
CC MIM; 602746; -
```

DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 3.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS00652; TNFR_NGFR_2; 2.
 DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 KW SIGNAL 1 38
 FT CHAIN 39 283
 FT
 FT DOMAIN 39 202
 FT TRANSMEM 203 223
 FT DOMAIN 224 283
 FT DOMAIN 224 162
 FT REPEAT 42 75
 FT REPEAT 78 119
 FT REPEAT 121 162
 FT DISULFID 42 53
 FT DISULFID 54 67
 FT DISULFID 57 75
 FT DISULFID 78 93
 FT DISULFID 96 111
 FT DISULFID 99 119
 FT DISULFID 121 127
 FT DISULFID 138 162
 FT CARBOHYD 110 110
 FT CARBOHYD 173 173
 FT CONFLICT 17 17
 SQ SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;

Query Match 15.1%; Score 246; DB 1; Length 283;
 Best Local Similarity 35.4%; Pred. No. 1.7e-12;
 Matches 69; Conservative 16; Mismatches 88; Indels 22; Gaps 8;

QY 7 PGLSLCLVLPAL---LPVPAVRGVAETPTYPWRDAETGERLVCAQCPGTFVORPCR 63
 Db 16 PKTDVLRVLVLTFLGAPCYAPALPSCKE-DEYP-----VGSE-CCPKCSPGYRVKEACG 68
 QY 64 RSPTTCGCPPPHYTFQWNYLER---CRYCNVLCGEREEARACHATHNRACRRTGFF 120
 Db 69 ELTGTCVCEPCPTGYAHLNGLSKLQCCQMCDPAMGLR--ASRNCSTENAVCGCSFGHF 126
 QY 121 A-----HAGFLEHASCPPGAGVIAPGTPSQNTQCPGPTFSASSSSSECCQPHRNC 174
 Db 127 CIVQDGDHCAACRAYATSSPGQVRQGGTESQTLQNCPPGTFPS-PNGTLEECQHQTKC 185
 QY 175 TALGLALNVPSSSH 189
 Db 186 SWLVTRKAGAGTSSSH 200

RESULT 7
 VT2_SFVKA
 ID VT2_SFVKA STANDARD; PRT; 325 AA.
 AC P25943;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS Shope fibroma virus (strain Kasza) (SFV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Leporipoxvirus.
 OX NCBI_TaxID=10272;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87321103; PubMed=2820128;
 RA Upton C., Delange A.M., McFadden G.;
 RT "Tumorigenic poxviruses; genomic organization and DNA sequence of the
 RL telomeric region of the Shope fibroma virus genome."; Virology 160:20-30(1987).
 RN [2]

RP FUNCTION.
 RX MEDLINE=91207415; PubMed=1850261;
 RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
 RA McFadden G., Goodwin R.G.;
 RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
 form of the TNF receptor";
 RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
 CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: M17433; -; NOT_ANNOTATED_CDS.
 DR EMBL: A23727; CAA01687.1; -;
 DR PIR: B43692; B43692.
 DR HSSP: P19438; ITNR.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00652; TNFR_NGFR_2; 1.
 KW Receptor; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 325
 FT DOMAIN 27 186
 FT REPEAT 27 62
 FT REPEAT 63 104
 FT REPEAT 105 147
 FT REPEAT 148 186
 FT CARBOHYD 105 105
 FT CARBOHYD 181 181
 FT CARBOHYD 205 205
 FT CARBOHYD 238 238
 SQ SEQUENCE 325 AA; 35132 MW; 81053039198A71E CRC64;

Query Match 14.5%; Score 236.5; DB 1; Length 325;
 Best Local Similarity 29.9%; Pred. No. 1.1e-11;
 Matches 58; Conservative 25; Mismatches 94; Indels 17; Gaps 4;

QY 11 LLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPGTFVORPCRDSPTTC 70
 Db 8 LVCVVYVYGDVFPYSSNQKCGGHY-----EKDGLCCASCHPGFYASRLCGPGSNTVC 61
 QY 71 GPCPPHYTFQWNYLERCRYCNVLCGEREEARACHATHNRACRRTGFFA-----HAG 124
 Db 62 SPCEGTFTASTNHAFACVSCRGPCGTHLSEQPCDTHDRVCNCSGTNYCLLKQNGCR 121
 QY 125 FCEHASCPPGAGVIAPGTPSQNTQCPGPTFSASSSSSECCQPHRNCATLGLALNVP 184
 Db 122 ICAPQTKCPAGYGV-SGHTFRAGDTLCEKCPHYSDLSLPTERCSTSFNIVSGFNL--- 177
 QY 185 GSSSHDTLCTSCGT 198
 Db 178 -YPVNETSCTTTAG 190

RESULT 8
 OX40_HUMAN
 ID OX40_HUMAN STANDARD; PRT; 277 AA.
 AC P43489; Q13663;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

```

Db      60 QNTVRCPGPGFVNDVVSSKPKCKTWCNLSRG--SERKQLCTATQDTVCRCRAG----- 112
Qy     124 GFCLEHASCPPGAGVIAPGTPSQNTQCPGPTFSASSSSSEOCOPHRNCTALGLALNV 183
Db     113 --TQPLDSYKPG-----VDCAPCPGPHF--SPGDNQACKPWTNCTLAGKHTLQ 156
Qy     184 PGSSSHDTLCHVS---CHGFPFLSTRVPGAEECERAVIDFVAFQDISIKRLQLLQALEAPE 240
Db     157 PASNSSDAICEDRDPPTAQPOGTQPPARPI-----TVQPT 193
Qy     241 GW-----GPTPR-----AGRAALQKLRRRLTELLGLRADGALLVRLLOALRVARMP 286
Db     194 AWPRTSQGPSTPRVEVPGGRAVAAILGLVLGLLGPL--AILLALYLLLRDQRLP 247

RESULT 9
VT2_MXXVL
ID_VT2_MXXVL STANDARD; PRT; 326 AA.
AC P29825;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OX Leporipoxvirus.
OC NCBI_TaxID=31530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91335768; PubMed=1651597;
RA Upton C., Macen J.L., Schreiber M., McFadden G.;
RT "Myxoma virus expresses a secreted protein with homology to the tumor
RT necrosis factor receptor gene family that contributes to viral
RT virulence.";
RL Virology 184:370-382(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M95181; AAA46632.1; -
CC EMBL; A23729; CAA01688.1; -
CC PIR; A40566; GQV2ML.
CC HSPG; P19438; ITNR.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 2.
CC ProDom; PD000771; TNFR_C6; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Receptor; Glycoprotein; Repeat; Signal.
CC SIGNAL 1 16
CC CHAIN 17 326
CC DOMAIN 27 186
CC REPEAT 27 62
CC REPEAT 63 104
CC REPEAT 105 147
CC REPEAT 148 186
CC CARBOHYD 66 66
CC CARBOHYD 181 181
CC CARBOHYD 205 205
CC CARBOHYD 238 238
CC SEQUENCE 326 AA; 35208 MW; ABBF027B947292FF CRC64;
CC -----
CC TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
CC 4 X TNFR-CYS.
CC TNFR-CYS 1.
CC TNFR-CYS 2.
CC TNFR-CYS 3.
CC TNFR-CYS 4.
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC ABBF027B947292FF CRC64;

```

FT	D0AMIN	236	271		CYTOPLASMIC (POTENTIAL).
FT	D0AMIN	25	164		4 X TNFR-CYS.
FT	REPEAT	25	60		TNFR-CYS 1.
FT	REPEAT	61	102		TNFR-CYS 2.
FT	REPEAT	103	123		TNFR-CYS 3. (INCOMPLETE).
FT	REPEAT	124	164		TNFR-CYS 4.
FT	CARBOHYD	143	143		N-LINKED (GLCNAC..). (POTENTIAL).
SQ	SEQUENCE	271 AA;	29895 MW;		C06465136B16E821 CRC64;

Query Match		13.1%;	Score 214;	DB 1:	Length 271;
Best Local Similarity		30.1%;	Pred.No. 5.1e-10;		
Matches		59;	Conservative	23;	Mismatches 64; Indels 48; Gaps

Qy	10	SLIQLVLALPALLVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTTFVQRPCRDRSPTT 69	: :	: :	:
Db	10	AFLILGSLGVTKLNCVK-----SYHP-----SGHK--CCRCQPQGHGMVSRCDHTRDTV 58	: :	: :	:
Qy	70	CGCPPPRHYTFQWNY--LERCRVCNVLCGEREEAREACHATHNRACRCRTGFFAHAGFCL 127	: :	: :	:
Db	59	CHCPCPGFYEAENVYTCRKCTOCNHRSQ--SELKQNCTFTEDTVCOCR----- 105	: :	: :	:
Qy	128	EHASCPPGAGVIAPGT-PSONT-----QCQPCPPGPTFFSASSSSSEQCPHRNCTALGLA 180	: :	: :	:
Db	106	-----PGTPQRDSSHKLGVDCVCPGPHF--SPGSNQACKPWTNCTLSGKQ 150	: :	: :	:
Qy	181	LNPVGSSSHDTLC 193	: :	: :	:
Db	151	IRHPASNSLDTV 163	: :	: :	:

RESULT	11	
CD40_HUMAN	STANDARD;	PRT; 277 AA.
ID	CD40_HUMAN	
AC	P25942;	
DT	01-MAY-1992 (Rel. 22, Created)	
DD	01-MAY-1992 (Rel. 22, Last sequence update)	
DT	30-MAY-2000 (Rel. 39, Last annotation update)	
DE	CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)	
DE	(TUMOR NECROSIS FACTOR RECEPTOR 5).	
GN	TNFRSF5 OR CD40.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_TaxID=9606;		
[1]	SEQUENCE FROM N.A.	
RX	MEDLINE=89356608; PubMed=2475341;	
RA	Stamenkovic I., Clark E.A., Seed B.;	
RT	"A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas.";	
RT	EMBO J. 8:1403-1410(1989).	
[2]		
RP	3D-STRUCTURE MODELING OF 24-144.	
RX	MEDLINE=97189482; PubMed=9037712;	
RA	Bajorath J., Aruffo A.;	
RT	"Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40.";	
RT	Proteins 27:59-70(1997).	
[3]		
RP	3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.	
RX	MEDLINE=98266353; PubMed=9605317;	
RA	Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,	
RA	Zheng Z., Naismith J.H., Thomas D.;	
RT	"The role of polar interactions in the molecular recognition of CD40L with its receptor CD40.";	
RT	Protein Sci. 7:1124-1135(1998).	
CC	-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.	
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-!- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.	
CC	-!- SIMILARITY: CONTAINS A LA-NGRF/TNFR-TYPE CYSTEINE-RICH REGION.	
CC	-!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;	
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm"	

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X60592; CAA43045.1; -
 DR PIR; S04460; S04460.
 DR PDB; 1CDF; 01-APR-97.
 DR MIM; 109535; -
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
 KW 3D-structure. 1 19 POTENTIAL.
 FT SIGNAL. 1 19 POTENTIAL.
 FT CHAIN 20 277 CD40L RECEPTOR.
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 194 215 POTENTIAL.
 FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 187 4 X TNFR-CYS.
 FT REPEAT 25 60 TNFR-CYS 1.
 FT REPEAT 61 103 TNFR-CYS 2.
 FT REPEAT 104 144 TNFR-CYS 3.
 FT REPEAT 145 187 TNFR-CYS 4.
 FT DISULFID 26 37
 FT DISULFID 38 51
 FT DISULFID 41 59
 FT DISULFID 62 77
 FT DISULFID 83 103
 FT DISULFID 105 119
 FT DISULFID 111 116
 FT DISULFID 125 143
 FT DISULFID 153 153
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2CA45680 CRC64;

Query Match 12.9%; Score 211; DB 1; Length 277;
 Best Local Similarity 30.5%; Pred. No. 8.9e-10;
 Matches 46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;

QY 49 CAQCPGCTFVQRCRDSPTTCGCPPRHYTQFWNYLERC---RYCNVLGGEREEARAC 105
 DB 38 CSLCQPGQKLVSDCTETFECLPCGSEFLDTWNRETHCHQHKYCDPNLGLRVQKQKGS 97
 QY 106 HATHNRACRTRTGFFAH---GFLCHASCPGAGVIAPGTPSONTOCQCPGPTFSASS 162
 DB 98 ET--DTICICEGWHCTSEACSCVLRSGSPGFGVKQIATGVSDTICEPCPGVFSNVS 155
 QY 163 SSSEQQCPHRNCTALGLALNPVGSSSHDTLC 193
 DB 156 SAFEKCHPMTSCETKDLVQQAAGTKNTDVVC 186

RESULT 12

CD40_MOUSE
 ID CD40_MOUSE STANDARD; PRT; 289 AA.
 AC P27512;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
 GN TNFRSF5 OR CD40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92105763; PubMed=1370315;
 RA Torres R.M., Clark E.A.;
 RT "Differential increase of an alternatively polyadenylated mRNA
 species of murine CD40 upon B lymphocyte activation.";
 RL J. Immunol. 148:620-626(1992).
 RN [2]
 RP REVISIONS.
 RC STRAIN=BALB/C;
 RA Torres R.M.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Liver;
 RX MEDLINE=93094586; PubMed=1281194;
 RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
 RA Howard M., Cockayne D.A.;
 RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";
 RL J. Immunol. 149:3921-3926(1992).
 CC -|- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; M83312; AAB08705.1; -
 DR EMBL; M94126; AAA37404.1; -
 DR EMBL; M94129; AAA37404.1; JOINED.
 DR EMBL; M94128; AAA37404.1; JOINED.
 DR EMBL; M94127; AAA37404.1; JOINED.
 DR PIR; A46476; A46476.
 DR HSSP; P25942; 1CDF.
 DR MGD; MGI:88336; Tnftrsf5.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 289 CD40L RECEPTOR.
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 194 215 POTENTIAL.
 FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 187 4 X TNFR-CYS.
 FT REPEAT 25 60 TNFR-CYS 1.
 FT REPEAT 61 103 TNFR-CYS 2.
 FT REPEAT 104 144 TNFR-CYS 3.
 FT REPEAT 145 187 TNFR-CYS 4.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

Query Match 12.4%; Score 203; DB 1; Length 289;
 Best Local Similarity 31.1%; Pred. No. 3.9e-09;
 Matches 47; Conservative 19; Mismatches 77; Indels 8; Gaps 3;

QY 49 CAQCPGCTFVQRCRDSPTTCGCPPRHYTQFWNYLERC---RYCNVLGGEREEARAC 105
 DB 38 CDLCQPGSRULTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRCEPNOGLRVKKEGT- 96
 QY 106 HATHNRACRTRTGFFAH---HAGFCLHASCPGAGVIAPGTPSONTOCQCPGPTFSASS 162
 DB 97 -AESDTVCTCKEGHCTSKDCECAQHTPCIPGFGVEMATETTDTVCHPCPGVGFSSNQS 155

```

Query Watch      12.4%; Score 202; DB 1; Length 269;
Best Local Similarity 28.5%; Pred. No. 4.4e-09;
Matches 67; Conservative 20; Mismatches 122; Indels 26; Gaps 7;

QY 47 LVCAQCPGPFVORCRRDSPTTCGCPPHRYTQFN---YLCRCRYCNVLGRREREA- 102
      ||| ||| |
db 36 LCDCDLPGGKGLINDCTEVSKTCQSGKGFEJSTWNREKYCHHEGRYCNPNLGRIOSEG 95
      ||| ||| |

```


Search completed: May 10, 2002, 10:59:24
Job time: 333 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:52:31 ; Search time 24.1 Seconds
(without alignments)
948.231 Million cell updates/sec

Title: US-09-280-567-2
Perfect score: 1634
Sequence: 1 MRLEGPGLSLLCLVLALPA.....RVAMPGLRSVRERFLPVH 300

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	351.5	21.5	461	1 A35356	tumor necrosis fac
2	333.5	20.4	459	2 I48854	gene murine tumour
3	332.5	20.3	474	2 B38634	tumor necrosis fac
4	315	19.3	435	2 I54182	tumor necrosis fac
5	262.5	16.1	349	2 D72175	G2R protein - vari
6	262.5	16.1	349	2 D36858	gene G4R protein -
7	262	16.0	348	2 T28623	hypothetical prote
8	236.5	14.5	325	2 B43692	T2 protein - rabbi
9	226	13.8	277	2 I37552	OX40 homolog - hum
10	215	13.2	326	1 GQVZML	T2 protein - myxom
11	214	13.1	271	2 A27873	OX40 antigen precu
12	211	12.9	277	2 AG0771	B-cell activation
13	203	12.4	305	2 A46476	B cell-associated
14	198.5	12.1	272	2 I48700	gene ox40 protein
15	186.5	11.4	595	2 A42086	CD30 antigen precu
16	185	11.3	256	2 B32393	T-cell antigen 4-1
17	176	10.8	416	1 JN0006	nerve growth facto
18	175.5	10.7	427	1 GQHUN	nerve growth facto
19	174	10.6	255	2 I38426	lymphocyte activat
20	170	10.4	425	1 A26431	nerve growth facto
21	159.5	9.8	260	1 A46517	CD27 antigen precu
22	155.5	9.5	327	2 A46484	apoptosis-mediated
23	148.5	9.1	1574	2 T43954	MEG6 protein - ra
24	148	9.1	250	1 A49053	CD27 antigen precu
25	147.5	9.0	5376	2 T42215	zonadhesin - mouse
26	145	8.9	335	2 A40036	apoptosis-mediated
27	144	8.8	324	2 JC2395	Fas antigen precu
28	143.5	8.8	1299	2 T43251	furin (EC 3.4.21.7
29	143	8.8	1620	2 T27283	hypothetical prote

30	140	8.6	314	2	I37383	FAS soluble protei
31	137.5	8.4	454	1	GQMST1	tumor necrosis fac
32	135	8.3	2321	2	S78549	notch3 protein - h
33	133	8.1	493	2	JC5486	membrane glycoprot
34	129.5	7.9	1548	2	S34583	serine proteinase
35	128.5	7.9	3635	2	T10053	laminin alpha 5 ch
36	127	7.8	1192	2	S69000	laminin gamma 2 ch
37	125.5	7.7	461	1	GQRTT1	tumor necrosis fac
38	125.5	7.7	1255	1	A24571	protein-tyrosine k
39	124.5	7.6	1713	2	A55347	adhesive ligand ep
40	124.5	7.6	3106	1	S53868	laminin alpha-2 ch
41	123.5	7.6	455	1	GQHUT1	tumor necrosis fac
42	122.5	7.5	2824	2	T22759	hypothetical prote
43	120	7.3	1609	1	MMHUB2	laminin gamma-1 ch
44	120	7.3	2318	2	S45306	notch 3 protein - h
45	119.5	7.3	461	2	JC4302	tumor necrosis fac

ALIGNMENTS

RESULT 1

A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dover, Science 248, 1019-1023, 1990
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a
A:Reference number: A35356; MUID:90260639
A:Accession: A35356
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SMI>
A:Cross-references: GB:M32315; NID:9189185; PIDN:AAA59929.1; PID:9189186
R:Kohnho, T.; Brewer, M.T.; Baker, S.B.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
A:Reference number: A36475; MUID:91045991
A:Accession: A36475
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195, 'R', 197-461 <KOH>
A:Cross-references: GB:M55994; GB:M38549; NID:9339757; PIDN:AAA36755.1; PID:9339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellul
A:Reference number: A48416; MUID:91370690
A:Accession: A48416
A:Status: preliminary
A:Molecule type: mRNA: protein
A:Residues: 23-461 <DEN>
A:Cross-references: GB:S63368; NID:9235648; PIDN:AAB19824.1; PID:9235649
A:Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons
A:Reference number: A36007; MUID:90349572
A:Accession: A36007
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A:Cross-references: GB:M35857; NID:9339751; PIDN:AAA63262.1; PID:9339752
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor
A:Reference number: A23666; MUID:91056048
A:Accession: A23666
A:Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>

R:Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A:Reference number: A35010; MUID:90110215
 A:Accession: B35010
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-31 <ENG>
 R:Kuhmert, P.; Kemper, O.; Wallach, D.
 Gene 150, 381-386, 1994
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
 A:Reference number: 138094; MUID:95121934
 A:Accession: 138094
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-37 <RES>
 A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
 C:Genetics: GDB:TNFR2
 A:Gene: GDB:TNFR2
 A:Cross-references: GDB:125914; OMIM:191191
 A:Map position: lp36.2-lp36.2
 A:Introns: 26/3
 A>Note: the list of introns is incomplete
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F:40-76/Domain: NGF receptor repeat homology <NG1>
 F:78-119/Domain: NGF receptor repeat homology <NG2>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>
 F:262-279/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.5%; Score 351.5; DB 1; Length 461;
 Best Local Similarity 29.8%; Pred. No. 4.5e-19;
 Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;

QY 8 GLSLCLVLALPALLPVPVAVRGVATPTVPRDAETGE-----RLVCAQCPRG 55
 DB 13 GLELWAAHALPA-----QVATTPAP----EPGTCRLREYDQTAQCCSKSPG 60
 QY 56 FTVPQPCRRDSTTCGPPRRHYTFWNYLCRYCNVLCGEREAEARACHATHNRACRC 115
 DB 61 QHAKVCTKSTVDCSDSTYTTLWNVPECLSGSCSDQVETQACTREQNRICTC 120
 QY 116 RTGFFAHAG-----FCLHASCPCGAGVAPGTPTSONTOCOPCPPTGFSASSSSQCO 169
 DB 121 RFGWYCALSKQEGCLCAPLRKCRFGVGVARPGTETSDVVKPCAPGTFSTNTSTDICR 180
 QY 170 PHRNCTALGLALNVPGSSSHDPLCTSGTFPLSTRVPGAEEAECEARAVIDPFAFDISIKRL 229
 DB 181 PHQICNVVA----IFGNASMDAVCTSTS--PTRSNWAPGAVHLPPV-----STRSQHT 227
 QY 230 QRLQLALEAPE-----GWGCTPRA----GRAALQKLRRLRLLFELGADGALLVRLQLAQ 280
 DB 228 QPTPEPTAPSTPSFLLPMPGSPPAEGSTGDFALPGLVGLVGTAL-----GLLIIGVNCV 282
 QY 281 ----RVARMP-GLERSVRERFLP 298
 DB 283 IMTVQKKRPLCLQREAKVPHLP 304

RESULT 2
 148854
 gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
 C:Accession: 148854
 R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
 Mamm. Genome 5, 726-727, 1994

A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
 A:Reference number: I48854; MUID:95178848
 A:Accession: I48854
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-459 <RES>
 A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 20.4%; Score 333.5; DB 2; Length 459;
 Best Local Similarity 29.7%; Pred. No. 1e-17;
 Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;

QY 46 RLVCACCPGTVORPCRRDSTTCGPPRRHYTFWNYLCRYCNVLCGEREAEARAC 105
 DB 37 QMCCAKCPGQVKKFKNTKSTDTVCADCEASMYTQVNMQFRTCLSCSSCSTDQVETAC 96
 QY 106 HATHNRACRCRTGFF----AHAGF----CLEHASCPCGAGVAPGTPTSONTOCOPCPPTGTF 158
 DB 97 TKQONRVCAACEAGRYCALXTHSGSCRCQCHRLSKCGFGVASSRAPNGNVLCACAPGTF 156
 QY 159 SASSSSQEQCPHRNCTALGLALNVPGSSSHDPLCT----SCGFFPLSTRVPGAEECERA 214
 DB 157 SDTTSSTDVCRPHRICSIILA----IPGNASTDAVCAPESPTLSAIPRTLIVYSQPEPTRSQ 212
 QY 215 VIDFVAFODISIKRLORLQALEAPGSGWGP-----RAGRAALQKLRRLRLLTELGAQD 269
 DB 213 PLD-----QEPGSPQTSFILTSL-----GSTPIEOTGKGISLPIGLIVGVTSL----- 257
 QY 270 GALLVRLQLAL----RVARMPGLERSVRERFLP 298
 DB 258 GLLMLGLVNCFLVQRKKPKSCLOQDAKVPHPV 290

RESULT 3
 B38634
 tumor necrosis factor receptor type 2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C:Accession: B38634; A40254; S54816
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
 A:Reference number: A38634; MUID:91187885
 A:Accession: B38634
 A:Molecule type: mRNA
 A:Residues: 1-474 <LEW>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
 Mol. Cell. Biol. 11, 3020-3026, 1991
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
 A:Reference number: A40254; MUID:91246168
 A:Accession: A40254
 A:Molecule type: mRNA
 A:Residues: 1-474 <GOO>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Kisssonergis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y.
 submitted to the EMBL Data Library, May 1995
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor
 A:Reference number: S54816
 A:Accession: S54816
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <KIS>
 C:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: cytokine receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F:40-77/Domain: NGF receptor repeat homology <NG1>
 F:79-120/Domain: NGF receptor repeat homology <NG2>

F:166-203/Domain: NGF receptor repeat homology <NG4>

```

Query Match          20.3%; Score 332.5; DB 2; Length 474;
Best Local Similarity 29.7%; Pred. No. 1.2e-17;
Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

QY 46 RLVCACQCPGCTFVQPCRRDSTTCGCPRRHYTQFWNYLERCRYCNVLCGEREEARAC 105
DB 52 QMCCAKCPGQVYKFCNKSTDTVCADCEASMYTQWNOFRCLSSSCTTDOVEIRAC 111
QY 106 HATHNRCRCRTGFF---AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCPGPGTF 158
DB 112 TKQNRVACACAGRYCALKTHSGRCQRLSKCGFGVGSRAPNGNVLCKACAPGTF 171
QY 159 SASSSSQCOQPHRNTALGLALNVPGSSSDTLCT----SCTGFPLSTRVPGAECERA 214
DB 172 SDTTSSTDCVRPHRCSILA---IPGNASTDAVCAPESPTLSAIPRTLYVSOPEPTRSQ 227
QY 215 VIDFVAFODISIKRLQRLQALEAPEGWGTP-----RAGRAALQKLRRRLTELLGAQD 269
DB 228 PLD---QSPGPSQTPSILTSL-----GSTPIIEQSTKGGISLPIGLIVGVTSL----- 272
QY 270 GALLVRLQAL----RVARMPLGLSVRERFLP 298
DB 273 GLLMLGLVNCIILVQRKKKPSCLORDAKVPHVP 305

RESULT 4
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A:Reference number: I54182; MUID:93352381
A:Accession: I54182
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

```

```

Query Match          19.3%; Score 315; DB 2; Length 435;
Best Local Similarity 31.8%; Pred. No. 2.3e-16;
Matches 89; Conservative 29; Mismatches 120; Indels 42; Gaps 12;

QY 3 ALEGPGLSLLCLVLPALLPVPVGVGVAETPTY-----PWRDA-----ETGERLYCAQC 52
DB 6 ATSAFGLANGPLVLGFLGLAASQPAV---PPYASENOTCRDQEKYEYEPQHRICCSRC 62
QY 53 PPGTFVQPCRRDSTTCGCPRRHYTQFWNYL---ERCRCYNVLCGEREEARACHATH 109
DB 63 PPGTYVSACRSIRDTVCATCAENSYNHWNLTICQLCRCPDPVNG--LEETAPCTSKR 120
QY 110 NRACRCRTGFFAHAGFCLF---H---ASCPPGA-GVIAGTFSQNTQCPGPGTFSASS 162
DB 121 KTCRCQCPGMFC-AAWALCTHCELLSDCPGTEAELKDEVGKGNHNCVPCKAGHFQNTS 179
QY 163 SSSECOQPHRNTALGLALNVPGSSSDTLCTSGCTGFPLSTRVPGAECERAVIDFVAFQ 222
DB 180 SPFARCPQHTRCENQGLVBAAPGTAQSDTCKNPLE-PLPPMSGTMMLAVLLPLAFL 238
QY 223 DIS-----IKRLQRLQALEAPEGWGTPPRAG 249
DB 239 LLATVFCIWKSHSPSLCKRLGSLK--RPPQEGPNPVAG 276

```

```

RESULT 5
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C>Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C:Accession: D72175
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lo
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola m
A:Reference number: A72150
A:Accession: D72175
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: G2R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match          16.1%; Score 262.5; DB 2; Length 349;
Best Local Similarity 30.0%; Pred. No. 1.6e-12;
Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;

QY 9 LSLCLVLALPALLPVPVGVGVAETPTYPMWRDAETGERLYCAQCPCGTFVQPCRRDSPT 68
DB 10 LFLSCIIINGRDAAPYTPPNCKCKDTEY-----KRHLNCLSCPPGCTYASRLCDSKTNT 63
QY 69 TCQPCPRHYTQFWNYLERCRYCNVLCGEREEARACHATHNRCRCRTGFF-----AH 122
DB 64 QCTPGSGTFTSRNNHLPACLSGRCNSQVETRSNTTHNRICEGSPGYCLLKSSG 123
QY 123 AGCLEHASCPPGAGVIAPGTPSQNTQCPGPGTFSASSSSSECOQPHRNTALGLALN 182
DB 124 CKACVSGTQCGIGYGV-SGHTSGVDVICSPCGFGTGYTSYTVSDTKCEPVNNTFNIDVE 182
QY 183 VPGSSSHDITLCTSGTGFPLSTRVPGA 209
DB 183 ITLVPVNDTSCRTTTTGLSESLTSE 209

RESULT 6
D36858
gene G4R protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
A:Reference number: A36859
A:Reference number: A36859
A:Accession: D36858
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhalov, A.A.; Blinov, V.M.; Gutorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H
A:Reference number: S46888
A:Accession: S46888
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <NOL>
A:Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protect

```

A:Reference number: S32385; MUID:93202281
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SNC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967,
C:Genetics:
A:Gene: GAR

C; Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F; 32-66/Domain: NGF receptor repeat homology <NGF> .
F; 68-109/Domain: NGF receptor repeat homology <NG2>
F; 110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 16.1%; Score 262.5; DB 2; Length 349;
Best Local Similarity 30.0%; Pred. No. 1.6e-12;
Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;

QY 9 LSLCLVLALPALLPVPAVGVAEPTYPWRDAETGERLVCACPPGTFVQRCDRSP 68
| | : :: - | : : | - | | | | : | : |
Db 10 LFLSCIINGRDAAPTYTPNGCKDTEY-----KRNLCCISCPPGYASRLCDSKNT 63

QY 69 TCGPCPPRHYTQFWNYLERCRYCNVLGGEREEEARACHATHNRACRGTGFF-----AH 122
 ||| :| | | | | : | | : | | | | | : | :
 Db 64 OCTPCGGSGTFSRNHLPLACLSNGRCNSNOVETRSNCTTHNRICECPGYCILLKGSSG 123

Qy 123 AGFCLHASCPGAGVIAPTSPNTQCPCPPGTFSASSSSSEQCQPHRNCTAIGLALN 182
- - - - : : : : | | | | : : : :
Dd 124 CKACVSOTKCGIYGV-SGHTSVGDVICSPCGGTGYSHTVSSADKCEPVNPNTFNVIDVE 182

```

Qy 183 VPGSSHDTLCTCTCGFPLSTRVPGAE 209
      : ||| | | || : |
Db 183 ITLYPVNDTCTRTTTTGLSESLTSE 209

```

RESULT 7
T28623

C/Species: variola major virus
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C/Accession: T28623

Nature 366, 748-751, 1993
A; Title: Potential virulence determinants in terminal regions of variola smallpox virus
A; Reference number: Z20488; PMID:94088747

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-348 <MAS>

A; Cross-references: ENBL:L2579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A; Experimental source: strain Bangladesh 1975
C; Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 16.0%; Score 262; DB 2; Length 348;
Best Local Similarity 30.8%; Pred. No. 1.7e-12;
Matches 64; Conservative 28; Mismatches 100; Indels 16; Gaps 4;

QY 9 LSLCLLVALPALLPVPVAVGVAEETYPWRDAE-TGERLVCAQCPCPTFVQRCRRDSP 67
| | : | | | : | | | | | : | | :
Db 10 LFLSCIINGRDAPYTP-----PNGKCKDTEYKRHNLCCLSCPCPTYASRLCDSKTN 61

Qy 68 TTCGCPPRHYTQFNWYLCRCRYCNVLCGEREEEAACHATHNRACRCRTGFF-----A 121
| | | | : | | | | : | | | | | | | | :
Db 62 TQCTPGSGGTFTRNNHLPACLSNGRCNSQVETSCNTTHNRICEGSPGYVCLLKGS 121

Qy 122 HAGFCLEHASCPPGAGVIAPGTSPQNTQCPCPPGTFSSASSSEQCQPHRNCTALGLAL 181
:-: |:-: |:-: |:-: |:-: |:-: |:-: |:-: |:-: |:-: |:-: |:-: |:-: |:-: |:-: |:-: |:-:
Db 122 GCKACVSTKCGTGYGV-SGHTSVGDVICPFCGGFTYSHTVSSADKCEPVNNTFNIDV 180

Qy 182 NPGSSHDTLCTSGTGFPLSTRVPGA 209
 : : || | | : : : :
 DQ 181 EITLYPNDTSTRTTTTGLSEILTSE 208

23

RESULT

B43692
 T2 protein - rabbit fibroma virus
 C:Species: rabbit fibroma virus, Shope fibroma virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: B43692
 R:Upton, C.; Delange, A.M.; McFadden, G.
 Virology 160, 20-30, 1987
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of t
 A:Reference number: A43692; MUID:87321103

A;Accession: B43692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-325 <OPT>

A; Cross-references: GB:M17433
C; Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F; 64-105/Domain: NGF receptor repeat homology <NG2>
F; 106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 14.5%; Score 236.5; DB 2; Length 325;
Best Local Similarity 29.9%; Pred. No. 1.3e-10;
Matches 58; Conservative 25; Mismatches 94; Gaps 4;
Indels 17;

Qy LLCLVLALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPEGTFVQPCRRDSPFTTC 70
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db LVCWVVYGDVPYSNNOGKCGGHDY-----EKDGLCCASCHGEFYASRLCGPGSNTVC 61

```

QY 71 GPCPPRIYTFWNYLERCRYCNVLGEEEEARACHATHNRACRRTFFA-----HAG 124
    ||  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 62 SPCEdGfETASTNHAPACVSCRGpCTGHLSPQCDRTHDRCVNCSTGNYCLLKQNGCR 121

```

QY 125 FCLEHACPPGAGVIAPGTPSQNTQCQPCPPGTFSSSSSSQCPHRCNTALGLNVP 184
 122 ICAPQTKCPAGVGV-SGHTFRAGDILCEKPPHTYSLSLSPTRCGTSFNYISVGFL--- 177

QY 185 GSSSHDTLCTCTG 198
::| ||: |
Db 178 -YPVNETSCTTAG 190

RESULT	9
I37552	
OX40 homoloa	- human

C; Species: homo sapiens (man)
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C; Accession: I37552
R; Latza, U.; Durkop, H.; Schnitzler, S.; Ringeling, J.; Eitelbach, F.; Hummel

Eur. J. Immunol. 24, 677-683, 1994
 A; Title: The human OX40 homolog: cDNA structure, expression and chromosomal
 A; Reference number: I37552; MUID:94170844

A; Residues: 1-277 <RES>
A; Molecule type: mRNA
A; Status: preliminary; translated from GB/EMBL/DBJ
Accession: 137554

A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CA53576.1; PID:g473958
C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 13.8%; Score 226; DB 2; Length 277;
Best Local Similarity 27.0%; Pred. No. 6.6e-10;

QY	6	GPGLSLLCLVLALPALLPPAVRGVAAETPTYPWRDAETGERLVCAQCPPGTFVQRCDR	65
DH	11	CPCAAIIITCTCISSMYRCIHCY-----CNYGVGNDR-----CAHQCBQDANCVCQSCDS	50

QY 66 SPTTCGCPPHRYTQFWNY--LERCRCYNVLGGEREEERACHATHNRACRCTRGFHAH 123
| | | | | : | | | : | | | : | | |
dN 60 ANNVVPCGCCDCAENAVNNVSCFDDKDFMCUNY DSG--SEBKV CSTATQNTVVCDBAC----- 112

QY 124 GFCLEHASCPPGAGVIAPCTPSONTOCQPCPGTFFSASSSSSEOCOPHRNCTALGLALNV 183
Db 113 --TQPLDSTKPG-----VDCAPCPGGHF--SPGDNOACKPWTNCTLAGKHTLQ 156
QY 184 PGSSSHDTLCTS---CTGFPLSTRVPGABECERAVIDFAFQDISIKRLQRLQALEAPE 240
Db 157 PASNSSDAICEDRDPTATQETQGGPARPI-----TVQPT 193
QY 241 GW-----GTPPR-----AGRAALQLKRLRLTELLGAQDQCALLVRLQLARVARMP 286
Db 194 AWPTSGPSTRVVEVPGGRAVAAILGLVLGLLGLPL--AAILLALYLLRRDQRLP 247
RESULT 10
GQVZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: A40566
R:Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virolgy 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A:Reference number: A40566; MUID:91335768
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <UPT>
A:Cross-references: GB:M95181; GB:M37976; NID:9332309; PIDN:AAA46632.1; PID:g332310
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C:Keywords: glycoprotein
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.2%; Score 215; DB 1; Length 326;
Best Local Similarity 29.3%; Pred. No. 5.1e-09;
Matches 58; Conservative 22; Mismatches 96; Indels 22; Gaps 5;
QY 12 LCILVLALPALL-----PVPARGVAETPTYPWRDAETGERLVCAQCPGTFVORPCRRDS 66
Db 4 LTLLEYACVYGGGAPYGADRGKRGNDY-----EKDGLCTSCPPGSGYASRLCGPGS 57
QY 67 PTCGCPPRHYTOFWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFFA----- 121
Db 58 DTVCSCKNETFTASTNHAPACVSCGRCTGHLSEQSCKDTRDVCDSAGNYCILLKQ 117
QY 122 -HAGFLEHASCPPGAGVIAPCTPSONTOCQPCPGTFFSASSSSSEOCOPHRNCTALGLA 180
Db 118 EGCRCAPKTKCPAGXGV-SGHRTRGDVLCTKCPRTYSDAVSSTETCTSSFNVISVEFN 176
QY 181 LNVPGSSSHDTLCTSTG 198
Db 177 L-----YPVNDTCTTTAG 190
RESULT 11
Ox40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12783; S08036
R:Walllett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC Ox40 antigen of activated CD4 positive T lymphocyte
A:Reference number: S12783; MUID:90214614
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <MAT>
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-271/Product: Ox40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TM>
Query Match 13.1%; Score 214; DB 2; Length 271;
Best Local Similarity 30.1%; Pred. No. 5.1e-09;
Matches 58; Conservative 23; Mismatches 64; Indels 48; Gaps 9;
QY 10 SLCLVLALPALLPVPARGVAETPTYPWRDAETGERLVCAQCPGTFVORPCRRDSPTT 69
Db 10 AFLLLGLSLGVTVKLNCVK-----DTYP-----SGHK-CCRECQPGHGMVSRCDHTRDTV 58
QY 70 CGPCPPRHYTOFWNY--LERCRCYCNVLCGEREEARACHATHNRACRCRTGFFAAGFCL 127
Db 59 CFCEPGFYNEAVNYDTCKQCTQCNRHG--SELKQNTPTEDTVCCOR----- 105
QY 128 EHASCPPGAGVIAPGT-PSQNT-----CQPCPPGTFSSASSSSSEOCOPHRNCTALGLA 180
Db 106 -----PGTQPRDSSSHKLGVDVCPGPGHF--SPGSNOACKPWTNCTLSGKQ 150
QY 181 LNVPGSSSHDTLCT 193
Db 151 IRHPASNSLDTVC 163
RESULT 12
A60771
B-cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A:Reference number: S04460; MUID:89356608
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R:Brasch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-
A:Reference number: A60771; MUID:89093941
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 211; DB 2; Length 277;
Best Local Similarity 30.5%; Pred. No. 8.8e-09;
Matches 46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;
QY 49 CAOCPPGTFVORPCRRDSPTTCGCPPRHYTOFWNYLRC-----RYCNVLCGEREEARAC 105
Db 38 CSLCQPGQKLVSCTETETECPLCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKQGS 97
QY 106 HATHNRACRCRTGFFAFAH-----GFLCHASCPGAGVIAPCTPSONTOCQPCPGTFFSASS 162
Db 98 ET--DTICTCEEHCTSEACESCVLHRSCTPGFGVKQIATGVSDTICEPCVPGFFSNVS 155

Db 10 LLFLGALRAFPQDRPFEDTCHGNPSHY---DKAVRCCYRCPMGLFTQOCQ-RPTDC 65
Qy 71 -GPCPPRHYTOFWNYLERCRYCNVLCGERE-EARACHATHNRACRRTGFFAHAGF--- 125
Db 66 RKQCEPDYLL---DEADRCTAC-VTCRDDLVEKTPCAWNSSRVCECRPGMFCSTSAVNS 121
Qy 126 ---CLEHASCPCGAGVIAPCTPSONTQOCOPCPGTFSASSSSSEOCQ-----PHRNCT 175
Db 122 CARCFHSVCPAGMIVKFPGTAKNTVCEPAPGV-SPACASPENCKEPSSSGTIPQAKPT 180
Qy 176 ALGLALNVFGSSSHDTL 192
Db 181 PVS-----PATSSASTM 192

Search completed: May 10, 2002, 10:54:20
Job time: 109 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:52:31 ; Search time 22.98 Seconds
(without alignments)
293.777 Million cell updates/sec

Title: US-09-280-567-2
Perfect score: 1634
Sequence: 1 MRALGPGLSLLCLVLALPA.....RVARMPGLRSVRERFLPVH 300

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1634	100.0	300	2	US-08-794-796-2
2	1619.5	99.1	299	4	US-09-286-529-17
3	1177	72.0	211	4	US-09-286-529-20
4	841	51.5	153	4	US-09-286-529-2
5	444	27.2	401	3	US-08-974-022-6
6	444	27.2	401	4	US-09-042-785A-12
7	444	27.2	401	4	US-08-795-445A-6
8	444	27.2	401	4	US-08-795-447A-6
9	444	27.2	401	4	US-08-974-186-6
10	444	27.2	401	4	US-08-795-446B-6
11	444	27.2	401	4	US-09-153-927-1
12	425.5	26.0	401	3	US-08-974-022-2
13	425.5	26.0	401	4	US-08-795-445A-2
14	425.5	26.0	401	4	US-08-795-447A-2
15	425.5	26.0	401	4	US-08-974-186-2
16	425.5	26.0	401	4	US-08-795-446B-2
17	424.5	26.0	401	3	US-08-974-022-4
18	424.5	26.0	401	4	US-09-042-785A-13
19	424.5	26.0	401	4	US-08-795-445A-4
20	424.5	26.0	401	4	US-08-795-447A-4
21	424.5	26.0	401	4	US-08-974-186-4
22	424.5	26.0	401	4	US-08-795-446B-4
23	353.5	21.6	461	4	US-09-042-785A-7
24	353.5	21.6	461	4	US-09-006-353A-4
25	351.5	21.5	461	1	US-08-385-229-2
26	351.5	21.5	461	2	US-08-650-000-2
27	351.5	21.5	461	4	US-08-477-347-3

28	351.5	21.5	461	4	US-08-476-862-2	Sequence 2, Appl1
29	351.5	21.5	461	6	5395760-2	Patent No. 5395760
30	346	21.2	227	3	US-08-974-022-48	Sequence 48, Appl1
31	346	21.2	227	4	US-08-795-445A-48	Sequence 48, Appl1
32	346	21.2	227	4	US-08-795-447A-48	Sequence 48, Appl1
33	346	21.2	227	4	US-08-974-186-48	Sequence 48, Appl1
34	346	21.2	227	4	US-08-795-446B-48	Sequence 48, Appl1
35	344	21.1	486	1	US-08-243-010-1	Sequence 1, Appl1
36	344	21.1	518	1	US-08-385-229-4	Sequence 4, Appl1
37	335	20.5	235	4	US-09-326-394-4	Sequence 4, Appl1
38	332.5	20.3	474	2	US-08-650-000-4	Sequence 8, Appl1
39	332.5	20.3	474	4	US-09-042-785A-8	Sequence 5, Appl1
40	332.5	20.3	474	6	5395760-4	Patent No. 5395760
41	318	19.5	163	2	US-08-219-237B-5	Sequence 5, Appl1
42	318	19.5	163	4	US-08-477-347-13	Sequence 13, Appl1
43	318	19.5	163	4	US-08-476-862-4	Sequence 4, Appl1
44	318	19.5	163	4	US-08-468-560C-5	Sequence 5, Appl1
45	316	19.3	164	2	US-08-232-087A-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-08-794-796-2
; Sequence 2, Application US/08794796
; Patent No. 5885800
; GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,796
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH50000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-794-796-2

Query Match 100.0%; Score 1634; DB 2; Length 300;

Best Local Similarity 100.0%; Pred. No. 1.9e-127;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAEGPGLSLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQR 60
DB 1 MRAEGPGLSLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQR 60
QY 61 PCRRDSPITTCGPPRRHYTQFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
DB 61 PCRRDSPITTCGPPRRHYTQFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
QY 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSSSSSEQCQPHRNCNTALGLA 180
DB 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSSSSSEQCQPHRNCNTALGLA 180
QY 181 LNVPGSSSHDITLCTSGTGFPLSTRVPGAECEERAVIDFVAFODISIKRLQLLQALEAPE 240
DB 181 LNVPGSSSHDITLCTSGTGFPLSTRVPGAECEERAVIDFVAFODISIKRLQLLQALEAPE 240
QY 241 GWGPTPRAGRAALQLKRRRLTELLGAODGALLVRLQLQALRVARMPGLSRRERFLPVH 300
DB 241 GWGPTPRAGRAALQLKRRRLTELLGAODGALLVRLQLQALRVARMPGLSRRERFLPVH 300
RESULT 2
US-09-286-529-17
; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-17

Query Match 99.1%; Score 1619.5; DB 4; Length 299;
Best Local Similarity 99.7%; Pred. No. 3e-126;
Matches 299; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MRAEGPGLSLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQR 60
DB 1 MRAEGPGLSLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQR 60
QY 61 PCRRDSPITTCGPPRRHYTQFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
DB 61 PCRRDSPITTCGPPRRHYTQFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
QY 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSSSSSEQCQPHRNCNTALGLA 180
DB 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSSSSSEQCQPHRNCNTALGLA 179
QY 181 LNVPGSSSHDITLCTSGTGFPLSTRVPGAECEERAVIDFVAFODISIKRLQLLQALEAPE 240
DB 180 LNVPGSSSHDITLCTSGTGFPLSTRVPGAECEERAVIDFVAFODISIKRLQLLQALEAPE 239
QY 241 GWGPTPRAGRAALQLKRRRLTELLGAODGALLVRLQLQALRVARMPGLSRRERFLPVH 300
DB 240 GWGPTPRAGRAALQLKRRRLTELLGAODGALLVRLQLQALRVARMPGLSRRERFLPVH 299
RESULT 3
US-09-286-529-20
; Sequence 20, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:

APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286.529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 211
TYPE: PRT
ORGANISM: Homo sapien
US-09-286-529-20

Query Match 72.0%; Score 1177; DB 4; Length 211;
Best Local Similarity 99.0%; Pred. No. 6.1e-90;
Matches 208; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MRAEGPGLSLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQR 60
DB 1 MRAEGPGLSLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQR 60
QY 61 PCRRDSPITTCGPPRRHYTQFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
DB 61 PCRRDSPITTCGPPRRHYTQFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
QY 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSSSSSEQCQPHRNCNTALGLA 180
DB 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSSSSSEQCQPHRNCNTALGLA 180
QY 181 LNVPGSSSHDITLCTSGTGFPLSTRVPGAE 210
DB 181 LNVPGSSSHDITLCTSGTGFPLSTRVPGEP 210

RESULT 4
US-09-286-529-2
; Sequence 2, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
US-09-286-529-2

Query Match 51.5%; Score 841; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.1e-62;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 85 LERCRCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCPGAGVIAPGTP 144
DB 1 LERCRCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCPGAGVIAPGTP 60
QY 145 SONTQCPCPPGTFSSSSSEQCQPHRNCNTALGLALNVPGSSSHDITLCTSGTGFPLSTR 204
DB 61 SONTQCPCPPGTFSSSSSEQCQPHRNCNTALGLALNVPGSSSHDITLCTSGTGFPLSTR 120
QY 205 VPGAECERAVIDFVAFODISIKRLQLLQALE 237
DB 121 VPGAECERAVIDFVAFODISIKRLQLLQALE 153

RESULT 5
US-08-974-022-6

; Sequence 6, Application US/08974022
; Patent No. 6015938

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-6

Query Match 27.2%; Score 444; DB 3; Length 401;

Best Local Similarity 39.6%; Pred. No. 3.6e-29;

Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LCLVLALPALLPVAVRGVAET--PTYWRDAETGERLVCAQCPTGVQRCRRDST 68

Db 4 LCCAL---VFLDISIKWTQETFPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWT 60

QY 69 TCGPCPPRHVTOFWNYLRCRYCNVLCGEREEARACHATHNRACRRTGFFAHAGFCLE 128

Db 61 VCAPCPDHYTDSWHTSDCLYCSPVKELQYVKQECNTHNRVCECKEGRYLEIEFCLK 120

QY 129 HASCPCGAGVIAPGTPTSONTCQCPPTFSASSSSQCPHRCNTALGLALNVPSSS 188

Db 121 HRSCPPGFGVQAGTPTNVTCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180

QY 189 HDTLCTSGTGFPLSTRVPGAEE--CERAVIDF 218

Db 181 HDNI---CSGENSESTQKCGIDVTLCBEAFRF 209

RESULT 6

US-09-042-785A-12

; Sequence 12, Application US/09042785A

; Patent No. 6194151

; GENERAL INFORMATION:

; APPLICANT: Busfield, Samantha J

; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-09-042-785A-12

Query Match 27.2%; Score 444; DB 4; Length 401;

Best Local Similarity 39.6%; Pred. No. 3.6e-29;

Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LCLVLALPALLPVAVRGVAET--PTYWRDAETGERLVCAQCPTGVQRCRRDST 68

Db 4 LCCAL---VFLDISIKWTQETFPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWT 60

QY 69 TCGPCPPRHVTOFWNYLRCRYCNVLCGEREEARACHATHNRACRRTGFFAHAGFCLE 128

Db 61 VCAPCPDHYTDSWHTSDCLYCSPVKELQYVKQECNTHNRVCECKEGRYLEIEFCLK 120

QY 129 HASCPCGAGVIAPGTPTSONTCQCPPTFSASSSSQCPHRCNTALGLALNVPSSS 188

Db 121 HRSCPPGFGVQAGTPTNVTCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180

QY 189 HDTLCTSGTGFPLSTRVPGAEE--CERAVIDF 218

Db 181 HDNI---CSGENSESTQKCGIDVTLCBEAFRF 209

RESULT 7

US-08-795-445A-6

; Sequence 6, Application US/08795445A

; Patent No. 6284485

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; APPLICANT: Lacey, David L.

; APPLICANT: Calzone, Frank J.

; APPLICANT: Chang, Ming-Shi

; TITLE OF INVENTION: OSTEOPROTEGERIN

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Angen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-6

Query Match 27.2%; Score 444; DB 4; Length 401;
Best Local Similarity 39.6%; Pred. No. 3.6e-29;
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LLCLVLALLPVPVAVGVAET--PTYPRDAETGERLVCAQCPTGTFVQPCRRDST 68
DB 4 LLCCAL---VFLDISIKWTQETFFPKYLYHDEETSHQLCDKCPPTGTYLKQCHTAKWKT 60

QY 69 TCGPCPPRHYTFWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFFAHAGFCLE 128
DB 61 VCAPCPDHVYTDWHTSDECLYCSVPVKELQYVKQECNTRNRCVCKEGRYLEIEFCLK 120
QY 129 HASCPPGAGVIAPGTPSNTQCPGPTFSASSSSSEOCQPHRNCNTALGLALNVPGSSS 188
DB 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180

QY 189 HDTLCTSCGFFPLSTRVPGAEE--CERAVIDF 218
DB 181 HDNI---CSGNSESTQKCGIDVTLCEEAFFR 209

RESULT 8

US-08-795-447A-6
Sequence 6, Application US/08795447A
Patent No. 6284728
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91362-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378D2

QY 11 LLCLVLALLPVPVAVGVAET--PTYPRDAETGERLVCAQCPTGTFVQPCRRDST 68
DB 4 LLCCAL---VFLDISIKWTQETFFPKYLYHDEETSHQLCDKCPPTGTYLKQCHTAKWKT 60

QY 69 TCGPCPPRHYTFWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFFAHAGFCLE 128
DB 61 VCAPCPDHVYTDWHTSDECLYCSVPVKELQYVKQECNTRNRCVCKEGRYLEIEFCLK 120

QY 129 HASCPPGAGVIAPGTPSNTQCPGPTFSASSSSSEOCQPHRNCNTALGLALNVPGSSS 188
DB 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180

QY 189 HDTLCTSCGFFPLSTRVPGAEE--CERAVIDF 218
DB 181 HDNI---CSGNSESTQKCGIDVTLCEEAFFR 209

Query Match 27.2%; Score 444; DB 4; Length 401;
Best Local Similarity 39.6%; Pred. No. 3.6e-29;
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LLCLVLALLPVPVAVGVAET--PTYPRDAETGERLVCAQCPTGTFVQPCRRDST 68
DB 4 LLCCAL---VFLDISIKWTQETFFPKYLYHDEETSHQLCDKCPPTGTYLKQCHTAKWKT 60

QY 69 TCGPCPPRHYTFWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFFAHAGFCLE 128
DB 61 VCAPCPDHVYTDWHTSDECLYCSVPVKELQYVKQECNTRNRCVCKEGRYLEIEFCLK 120
QY 129 HASCPPGAGVIAPGTPSNTQCPGPTFSASSSSSEOCQPHRNCNTALGLALNVPGSSS 188
DB 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180

QY 189 HDTLCTSCGFFPLSTRVPGAEE--CERAVIDF 218
DB 181 HDNI---CSGNSESTQKCGIDVTLCEEAFFR 209

Query Match 27.2%; Score 444; DB 4; Length 401;
Best Local Similarity 39.6%; Pred. No. 3.6e-29;
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LLCLVLALLPVPVAVGVAET--PTYPRDAETGERLVCAQCPTGTFVQPCRRDST 68
DB 4 LLCCAL---VFLDISIKWTQETFFPKYLYHDEETSHQLCDKCPPTGTYLKQCHTAKWKT 60

QY 69 TCGPCPPRHYTFWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFFAHAGFCLE 128
DB 61 VCAPCPDHVYTDWHTSDECLYCSVPVKELQYVKQECNTRNRCVCKEGRYLEIEFCLK 120
QY 129 HASCPPGAGVIAPGTPSNTQCPGPTFSASSSSSEOCQPHRNCNTALGLALNVPGSSS 188
DB 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-447A-6

Query Match 27.2%; Score 444; DB 4; Length 401;
Best Local Similarity 39.6%; Pred. No. 3.6e-29;
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LLCLVLALLPVPVAVGVAET--PTYPRDAETGERLVCAQCPTGTFVQPCRRDST 68
DB 4 LLCCAL---VFLDISIKWTQETFFPKYLYHDEETSHQLCDKCPPTGTYLKQCHTAKWKT 60

QY 69 TCGPCPPRHYTFWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFFAHAGFCLE 128
DB 61 VCAPCPDHVYTDWHTSDECLYCSVPVKELQYVKQECNTRNRCVCKEGRYLEIEFCLK 120
QY 129 HASCPPGAGVIAPGTPSNTQCPGPTFSASSSSSEOCQPHRNCNTALGLALNVPGSSS 188
DB 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180

QY 189 HDTLCTSCGFFPLSTRVPGAEE--CERAVIDF 218
DB 181 HDNI---CSGNSESTQKCGIDVTLCEEAFFR 209

RESULT 9

US-08-974-186-6
Sequence 6, Application US/08974186
Patent No. 6284740
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-186-6

QY 11 LLCLVLALLPVPVAVGVAET--PTYPRDAETGERLVCAQCPTGTFVQPCRRDST 68
DB 4 LLCCAL---VFLDISIKWTQETFFPKYLYHDEETSHQLCDKCPPTGTYLKQCHTAKWKT 60

QY 69 TCGPCPPRHYTFWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFFAHAGFCLE 128
DB 61 VCAPCPDHVYTDWHTSDECLYCSVPVKELQYVKQECNTRNRCVCKEGRYLEIEFCLK 120

QY 129 HASCPPGAGVIAPGTPSNTQCPGPTFSASSSSSEOCQPHRNCNTALGLALNVPGSSS 188
DB 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180

QY 189 HDTLCTSCGFFPLSTRVPGAEE--CERAVIDF 218
DB 181 HDNI---CSGNSESTQKCGIDVTLCEEAFFR 209

Query Match 27.2%; Score 444; DB 4; Length 401;
Best Local Similarity 39.6%; Pred. No. 3.6e-29;
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LLCLVLALLPVPVAVGVAET--PTYPRDAETGERLVCAQCPTGTFVQPCRRDST 68
DB 4 LLCCAL---VFLDISIKWTQETFFPKYLYHDEETSHQLCDKCPPTGTYLKQCHTAKWKT 60

QY 69 TCGPCPPRHYTFWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFFAHAGFCLE 128
DB 61 VCAPCPDHVYTDWHTSDECLYCSVPVKELQYVKQECNTRNRCVCKEGRYLEIEFCLK 120
QY 129 HASCPPGAGVIAPGTPSNTQCPGPTFSASSSSSEOCQPHRNCNTALGLALNVPGSSS 188
DB 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180

QY 189 HDTLCTSCGFFPLSTRVPGAEE--CERAVIDF 218
DB 181 HDNI---CSGNSESTQKCGIDVTLCEEAFFR 209

Query Match 27.2%; Score 444; DB 4; Length 401;
Best Local Similarity 39.6%; Pred. No. 3.6e-29;
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LLCLVLALLPVPVAVGVAET--PTYPRDAETGERLVCAQCPTGTFVQPCRRDST 68
DB 4 LLCCAL---VFLDISIKWTQETFFPKYLYHDEETSHQLCDKCPPTGTYLKQCHTAKWKT 60

QY 69 TCGPCPPRHYTFWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFFAHAGFCLE 128
DB 61 VCAPCPDHVYTDWHTSDECLYCSVPVKELQYVKQECNTRNRCVCKEGRYLEIEFCLK 120
QY 129 HASCPPGAGVIAPGTPSNTQCPGPTFSASSSSSEOCQPHRNCNTALGLALNVPGSSS 188
DB 121 HRSCPPGFGVQAGTPERTVCKRCPDGFNSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180

```

Query Match      27.2%   Score 444;   DB 4;   Length 401;
Best Local Similarity 39.6%;   Pred. No. 3.6e-29;
Matches         84;   Conservative 33;   Mismatches 86;   Indels 10;   Gaps 4;

QY    11  LLCLVLALPALLPPAVRGVAET--PTYPWRDAETGERLVCAQCPCPGTFVQRPCRDSPT 68
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     4  LCCAL---VFLDISIKWTTQTETPPKYLHYDEETSQLLCDKCPGTYLQAQCTAKWT 60

QY    69  TCGPCPPPHYTQFWNYLERGRYCNVLGEREEREARACHATHINRACRTGFFAHAGFLE 128
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61  VCAPCPDHYVTDSWHTSDECLYCSPVKCELOYKVQECNTRHNRYCKEGRYLETEFCLK 120

```

```

QY 129 HASCPPGAGVIAPGTSPONTQCPCPGTFTSASSSSSEOCQPHRNCTALGLNALNVPGSSS 188
      | ||||| ||: ||| :||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||:
Db 121 HRSCPPGFVGVQAGTPERNTVCKRCPDGFGFSNETSSKAPCRKHTNCVSFGLLLLTQKGNA 180
      ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 189 HDPLTCTSGCFPLSTRVPGAEE--CERAVIDF 218
      ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 181 HDNI---CSGNSESTOKCGIDVTLCCEAFFRF 209
      ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 11
US-09-153-927-1
; Sequence 1, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; APPLICANT: Zou, Jun
; TITLE OF INVENTION: A Method of Identifying Agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; TITLE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
US-09-153-927-1

Query Match          27.2%; Score 444; DB 4; Length 401;
Best Local Similarity 39.6%; Pred. No. 3.6e-29;
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LCLCVIALPALLPVPAVRGVAET--PTYPWDAETGERLVCAQCPPGTFTVQRCDRDSPT 68
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 LLCCAL---VFLDISIKWTTQTETFPFKYLHYDEETSHOLLCDKCPPGTYLKHCRTAKWK 60
      ||||| ||: ||| :||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||:

QY 69 TCQCPPRHVTQPNWLERCYNVLGREGREEARACHATHNRACRCRTGTFFAHAGFCLE 128
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 VCACPDPHYITDWSHTSDCLYCSPVKELQYVQBCNTRTHRVCECKEGRYLETEFCLK 120
      ||||| ||: ||| :||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||:

QY 129 HASCPPGAGVIAPGTSPONTQCPCPGTFTSASSSSSEOCQPHRNCTALGLNALNVPGSSS 188
      | ||||| ||: ||| :||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||:
Db 121 HRSCPPGFVGVQAGTPERNTVCKRCPDGFGFSNETSSKAPCRKHTNCVSFGLLLLTQKGNA 180
      ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 189 HDPLTCTSGCFPLSTRVPGAEE--CERAVIDF 218
      ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 181 HDNI---CSGNSESTOKCGIDVTLCCEAFFRF 209
      ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 12
US-08-974-022-2
; Sequence 2, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA

```

ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974.022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-2

Query Match 26.0%; Score 425.5; DB 3; Length 401;
Best Local Similarity 39.5%; Pred. No. 1.2e-27;
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;
QY 34 PTYPWRDAETGERLVCAOCPGTFVORPCRRDSPPTCGPCPPRHHTQFWNYLRCRYCNV 93
DB 26 PKYLHYDPETGRLQCDKCAPGTLYLKQCHTVRRKTLVPCPDYSYDTSNHTSDEVCYCS 85
QY 94 LCGEREERACHATHNRACRGTFFAHAGFCLHSCPPGAGVIAPCTPSONTCQCP 153
DB 86 VKELQTVKQECNRTHNRVCEEGRYLELEFCLHRSCPPGLVQLAGTPERTVCKRC 145
QY 154 PGFTSASSSECOQHNCRTALGLALNPGSSSHDTLCTSGTGFPLSTRVPGAE--C 211
DB 146 PDGFFSGTSSKAPCKKHTNCSLLGLLLQKGNATHDNV---CSGNREATQNCIGDVTLC 202
QY 212 ERAVIDFAFQDISIKRLQRLQAL 236
DB 203 EBAFFFAVPTKIIPNLSVLVDSL 227

RESULT 13
US-08-795-445A-2
Sequence 2, Application US/08795445A
Patent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795.445A
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-2

Query Match 26.0%; Score 425.5; DB 4; Length 401;
Best Local Similarity 39.5%; Pred. No. 1.2e-27;
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;
QY 34 PTYPWRDAETGERLVCAOCPGTFVORPCRRDSPPTCGPCPPRHHTQFWNYLRCRYCNV 93
DB 26 PKYLHYDPETGRLQCDKCAPGTLYLKQCHTVRRKTLVPCPDYSYDTSNHTSDEVCYCS 85
QY 94 LCGEREERACHATHNRACRGTFFAHAGFCLHSCPPGAGVIAPCTPSONTCQCP 153
DB 86 VKELQTVKQECNRTHNRVCEEGRYLELEFCLHRSCPPGLVQLAGTPERTVCKRC 145
QY 154 PGFTSASSSECOQHNCRTALGLALNPGSSSHDTLCTSGTGFPLSTRVPGAE--C 211
DB 146 PDGFFSGTSSKAPCKKHTNCSLLGLLLQKGNATHDNV---CSGNREATQNCIGDVTLC 202
QY 212 ERAVIDFAFQDISIKRLQRLQAL 236
DB 203 EBAFFFAVPTKIIPNLSVLVDSL 227

RESULT 14
US-08-795-447A-2
Sequence 2, Application US/08795447A
Patent No. 6284728
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Angen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91362-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795.447A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378D2
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-447A-2

	Query Match	26.0%;	Score 425.5;	DB 4;	Length 401;
	Best Local Similarity	39.5%;	Pred. No. 1.2e-27;		
	Matches	81; Conservative	33; Mismatches	86; Indels	5; Gaps
Qy	34	PTVWRDAETGERLVCACCPGTFVORPCRRDSPTTTCGPCPPRHYYTOFWNYLERCRYCNV	93		
Db	26	KYLLHYDPETGRQLLCDKCAPGYLKQHCTVRRKTLVCPDYSYTDSSHSTDECVYCSP	85		
Qy	94	LCSREBEARACHATHINNRACRRTGFHAGFLEHASCPPGAGVIAPTPSNTQCPCP	153		
Db	86	VCKELQTIVKECNRTHNRVCEBEGRYLELEFCCLKHRSCPPGLVLGVAQGTPERTNVCVKRC	145		
Qy	154	PPGTFASASSSSSQOCPHRNCTALGLALNVPGSSSHDTLCSTCGTGPLSTRVPGAEE--C	211		
Db	146	PDGFFSETSKAPCRKHMTNCSSGLLLLTQKNATHDNV---CSGNREATONGCIDVTLC	202		
Qy	212	ERAVIDVFVAFDISIKRLQRLLQAL	236		
Db	203	EEAFFFRFAVPTKIIPNWLSVLVDSL	227		

```

RESULT 15
US-08-974-186-2
; Sequence 2, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-186-2

```

```

Qy 94 LCGREBEARACHATHNRACR CRTGFFPAHAGFLEHUASCPGAGVATPGTPSONTOCQPC 153
    : | : | | | | : | : | | | | | | : | | | | | : |
Db 86 VKCELQTVKOB CNRTHNRVCEBEGRYLELEFC LKHRSCPPGLGVLAQAGTPERNVTCKRC 145

Qy 154 PPGTFSASSSSSEOCQPHRNCRTALGLALNVP GSSHDTLCTSGTGPPLSTRVPGASE--C 211
    | | | | | : | : | | | | | | : | : | : | : |
Db 146 PDGFFSETGTSKAPCRKHTNCSS LGLLLIQKNATHDNV---CSGNREATQNGIDVTLC 202

Qy 212 ERAVIDFVAFQDISIKRLQLLQAL 236
    | | | | | : | : | : | : |
Db 203 EEAFFRAVPTKIIPNWLVS LVDSL 227

```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:52:31 ; Search time 40.16 Seconds
(without alignments)
553.336 Million cell updates/sec

Title: US-09-280-567-2

Perfect score: 1634

Sequence: 1 MRALEGGLSLCLVLALPA.....RVARMPGLRSVRERFLPVH 300

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1634	100.0	300	19 AAW66102	Amino acid sequenc
2	1634	100.0	300	15 AAW63622	Human tumour necro
3	1634	100.0	300	20 AAY03099	Human lung TNF-rec
4	1634	100.0	300	20 AAY42182	Human FLINT #1 pro
5	1634	100.0	300	20 AAY17479	Mammalian tumour n
6	1634	100.0	300	20 AAY06817	Human DCR3 polyep
7	1634	100.0	300	20 AAW97749	Human tumour necro
8	1634	100.0	300	20 AAW95082	Orphan receptor (H
9	1634	100.0	300	21 AAB19335	A full length huma
10	1634	100.0	300	21 AAB28559	Human soluble TNF
11	1634	100.0	300	21 AAB24057	Human PRO212 prote

12	1634	100.0	300	21 AAB33416	Human PRO212 prote
13	1634	100.0	300	21 AAB03621	Human Fas ligand 1
14	1634	100.0	300	21 AAY97246	M88 TNF receptor r
15	1634	100.0	300	21 AAY90357	Human tumour necro
16	1634	100.0	300	21 AAB24395	Human PRO212 prote
17	1634	100.0	300	21 AAY96596	Human FLINT. Homo
18	1634	100.0	300	22 AAE03568	Human native fas 1
19	1634	100.0	300	22 AAB74466	Human FLINT native
20	1634	100.0	300	22 AAB71754	Human NTR3. Homo
21	1634	100.0	300	22 AAB48161	Human PRO212 poly
22	1634	100.0	300	22 AAB50903	Human PRO212 prote
23	1634	100.0	341	22 AAG73740	Human colon cancer
24	1620	99.1	300	21 AAY77458	Human TNF receptor
25	1619	99.1	300	21 AAB19710	Human Fas ligand 1
26	1619	99.1	300	21 AAY96597	Human FLINT. Homo
27	1619	99.1	300	22 AAE03570	Human fas ligand 1
28	1619	99.1	300	22 AAB83950	Amino acid sequenc
29	1619	99.1	300	22 AAB68045	Amino acid sequenc
30	1619	99.1	300	22 AAB68048	Amino acid sequenc
31	1610	98.5	302	20 AAY42183	Human FLINT #2 pro
32	1509	92.4	300	21 AAB03623	Human Fas ligand 1
33	1502	91.9	300	21 AAB03622	Monkey Fas ligand
34	1502	91.9	300	21 AAB03624	Human Fas ligand 1
35	1491	91.2	271	20 AAY42184	Human mFLINT #1 pr
36	1491	91.2	271	21 AAB19334	A mature human Fas
37	1491	91.2	271	21 AAB19705	Human Fas ligand 1
38	1491	91.2	271	21 AAY97247	M88 TNF receptor r
39	1491	91.2	271	21 AAY96598	Human mature fas 1
40	1491	91.2	271	22 AAE03567	Human mature fas 1
41	1491	91.2	271	22 AAB68044	Amino acid sequenc
42	1491	91.2	271	22 AAB68047	Amino acid sequenc
43	1491	91.2	271	22 AAB74465	Human FLINT mature
44	1487	91.0	271	21 AAB19709	Protease-resistant
45	1487	91.0	271	22 AAE03571	Human mature fas 1

ALIGNMENTS

RESULT 1

AAW66102

ID AAW66102 standard; Protein; 300 AA.

XX

AC AAW66102;

XX

DT 02-DEC-1998 (first entry)

XX

DE Amino acid sequence of tumour necrosis related receptor (TR4).

XX

KW Human; tumour necrosis related receptor; TR4; agonist; antagonist;

KW Inhibition; chronic; acute; inflammation; arthritis; septicaemia;

KW autoimmune disease; transplant rejection; stroke; cancer;

KW Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN EP861850-A1.

XX

PD 02-SEP-1998.

XX

PF 20-JAN-1998; 98EP-0300382.

XX

PR 04-FEB-1997; 97US-0794796.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Emery J, Tan KB, Trunch A, Young PR;

XX

DR WPI; 1998-508248/44.

XX

PT N-PSDB; AAV07654.

XX

PT New DNA encoding tumour necrosis related receptor - used to treat

PT and prevent e.g. inflammation, arthritis, septicaemia, autoimmune

PT diseases, transplant rejection, infection, stroke, ischaemia, ARDS,
 PT restenosis, AIDS, bone disorders and cancer
 PS Claim 1; Fig 1; 2lpp; English.
 XX
 CC This is the amino acid sequence of the human tumour necrosis related
 CC receptor (TR4), used in the method of the invention. The TR4 protein
 CC or its agonist can be used to treat a subject in need of enhanced
 CC TR4 polypeptide activity. The antagonist is used to inhibit TR4
 CC polypeptide activity. The active agents can be used for the
 CC treatment and prevention of diseases such as chronic and acute
 CC inflammation, arthritis, septicemia, autoimmune diseases, transplant
 CC rejection, stroke, cancer, Alzheimer's disease.
 XX
 XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 19; Length 300;
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRALGPGSLCLLCLVLPALLPVPVAVRGVAETPTYPWRDAETGERLYVCAQCPGCTFVQR 60
 DB 1 mralepgslcllclvlpallpvpvavrgvaetptypwrdaetgerlyvcaqcpptfvqr 60
 QY 61 PCRRDSPPTCGPPRHYTQFNWYLCRYCNVLCGEREEARACHATHNRCRCRTGFF 120
 DB 61 pcrdrspptcgpprhytqfnwylcrycnvlgereearachathnrcrcrtgff 120
 QY 121 AHAGFCLHASCPPGAGVIAPGTPSQNTQCPGPTFSASSSSSEQCPHNRCTALGLA 180
 DB 121 ahagfclhascppgagviapgtpsqntqcpptfsassssseqcqhnrctalgla 180
 QY 181 LNVPGSSSHDILCTSGTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQLLQALEAPE 240
 DB 181 lnpvgssshdiltctsgtgfplstrvpgaeeeceravidfvafqdisikrlqlqaleape 240
 QY 241 GWGPTPRAGRAALQKLRRRLTELLGADGALLVRLQLQALVARMPLGLSVRRERFLPVH 300
 DB 241 gwgptpragraalqklrrrtellgagdgallvrlqlqalvarmpglsvrrerflpvh 300

RESULT 2
 AAW63622
 ID AAW63622 standard; Protein; 300 AA.
 AC AAW63622;
 XX
 DT 26-OCT-1998 (first entry)
 XX
 DE Human tumour necrosis factor receptor-6 alpha protein.
 XX
 KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 beta;
 KW endothelial cells; keratinocytes; normal prostate; apoptosis;
 KW prostate tumour tissue.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..30
 FT Protein 31..300
 FT /note= "TNFR-6 alpha"
 FT Region 31..282
 FT /note= "Soluble extracellular domain"
 XX
 PN W09830694-A2.
 XX
 PD 16-JUL-1998.
 XX
 PF 13-JAN-1998; 98WO-US00153.
 XX
 PR 14-JAN-1997; 97US-0035496.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 PI Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;
 XX
 DR WPI; 1998-399142/34.
 DR N-PSDB; AAV39085.
 XX
 PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
 PT the diagnosis of immune system-related disorder(s)
 XX
 PS Claim 20; Fig 1; 9lpp; English.
 XX
 CC The present sequence represents the human tumour necrosis factor
 CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides
 CC for the TNFR-6 beta protein (AAW63623). TNFR-6 alpha and TNFR-6 beta
 CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs
 CC are expressed in endothelial cells, keratinocytes, normal prostate and
 CC prostate tumour tissue. For a number of disorders of these cells,
 CC particularly of the immune system, substantially altered (whether
 CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta
 CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
 CC polypeptides, nucleic acids and antibodies are claimed to be useful in
 CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
 CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are
 CC also claimed to be useful for identifying ligands which may be useful
 CC in the treatment of apoptosis related disorders.
 XX
 XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 19; Length 300;
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRALGPGSLCLLCLVLPALLPVPVAVRGVAETPTYPWRDAETGERLYVCAQCPGCTFVQR 60
 DB 1 mralepgslcllclvlpallpvpvavrgvaetptypwrdaetgerlyvcaqcpptfvqr 60
 QY 61 PCRRDSPPTCGPPRHYTQFNWYLCRYCNVLCGEREEARACHATHNRCRCRTGFF 120
 DB 61 pcrdrspptcgpprhytqfnwylcrycnvlgereearachathnrcrcrtgff 120
 QY 121 AHAGFCLHASCPPGAGVIAPGTPSQNTQCPGPTFSASSSSSEQCPHNRCTALGLA 180
 DB 121 ahagfclhascppgagviapgtpsqntqcpptfsassssseqcqhnrctalgla 180
 QY 181 LNVPGSSSHDILCTSGTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQLLQALEAPE 240
 DB 181 lnpvgssshdiltctsgtgfplstrvpgaeeeceravidfvafqdisikrlqlqaleape 240
 QY 241 GWGPTPRAGRAALQKLRRRLTELLGADGALLVRLQLQALVARMPLGLSVRRERFLPVH 300
 DB 241 gwgptpragraalqklrrrtellgagdgallvrlqlqalvarmpglsvrrerflpvh 300

RESULT 3
 AAY03099
 ID AAY03099 standard; Protein; 300 AA.
 AC AAY03099;
 XX
 DT 09-DEC-1999 (first entry)
 XX
 DE Human lung TNF-receptor protein.
 XX
 KW Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;
 KW detection; immunoassay; diagnosis; disease; immune system; tumour;
 KW osteogenic system; cardiovascular system; central nervous system; asthma;
 KW peripheral nervous systems; transplant incompatibility; antitumor;
 KW rheumatoid arthritis; antiasthmatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX

```

FH Key Location/Qualifiers
FT CDS 134..1036
FT /*tag= a
FT /product= "TNF-receptor"
XX
XX
XX
XX DE19809978-A1.
XX
XX 16-SEP-1999.
XX
XX PF 09-MAR-1998; 98DE-1009978.
XX
XX PR 09-MAR-1998; 98DE-1009978.
XX
XX PA (BADI ) BASE AG.
XX
XX PI Kroeger B;
XX
XX WPI: 1999-519473/44.
XX N-PSDB; AA209998.
XX
XX New soluble member of tumor necrosis factor receptor family, useful for
XX identification specific modulators and for treating disease e.g. tumors
XX
XX
XX Claim 1; Page 8-9; 10pp; German.
XX
XX This invention describes a novel tumour necrosis factor (TNF) receptor
XX (I) isolated from human lung tissue. (I) is used: (i) to raise specific
XX antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands
XX (A). potential therapeutic agents; and (iii) therapeutically (optionally
XX expressed from a gene therapy vector) in conditions associated with a
XX deficit of (I). Ab are used: (a) for qualitative or quantitative
XX detection of (I) in standard immunoassays (for diagnosis of disease, or
XX susceptibility, or for monitoring); and (b) as therapeutic inhibitors in
XX cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is
XX used: (A) for recombinant production of (I); (B) also its oligonucleotide
XX fragments, in standard hybridization and/or amplification assays; (C) as
XX source of antisense molecules or ribozymes; and (D) to produce transgenic
XX animals (for studying (patho)physiology of (I)). Diseases possibly
XX associated with under- or over-expression of (I) are those of the immune,
XX osteogenic, cardiovascular and central or peripheral nervous systems,
XX tumors, transplant incompatibility, asthma and rheumatoid arthritis. The
XX products of the invention have antitumor, antiasthmatic and
XX antiarthritic activity. This sequence represents the TNF-receptor of the
XX invention.
XX
XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.4e-122;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPSLCLVLALPVPVAVRGVAETPTVPRDAETGERLVCAQCPPGTFVOR 60
DB 1 mralegpslclvlalpvpavrgvaetptvprdaetgerlvcaqppgtfvqr 60
QY 61 PCRDSPTTCGPPPHYTFQWNYLERCYCNVLCGEREEARACHATHNACRRTGFF 120
DB 61 pcrdspttcgppphrhytfqwnylercycnvlgerееearachathnacrtrgff 120
QY 121 AHAGFCLHACPPGAGVYAPGPSQNTQCPCPGTFFSASSSSSQCPHNCRTALGIA 180
DB 121 ahagfclhascpvgagvylapgtspntqccpvgtfssassssqcpqhncrtalgi 180
QY 181 LNVPGSSHDTLCTGTFPLSTRVPGAECEERAVIDFVAFODISIKRLQRLQALEAPE 240
DB 181 lnvpgsshdltctgtgfpplstrvpgaeceeravidfvafodisikrlqrlqaleape 240
QY 241 GWGPTPRAGRAALQLKRLRLTELICAOQCALLVRLQLALRVARMPLGERSVRERFLPVH 300
DB 241 gwgptpragraalqlkrrrltelicaoqcallvrlqlalrvarmplgersvrerflpvh 300

RESULT 4
AA42182
ID AAY42182 standard; Protein; 300 AA.
XX
XX AC AAY42182;
XX
XX DT 17-DEC-1999 (first entry)
XX
XX DE Human FLINT #1 protein sequence.
XX
XX Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
XX apoptosis; inflammation; cancer; diabetes; acute liver failure;
XX sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
XX reperfusion-associated injury; aplastic anaemia; differentiation;
XX growth; myelodysplastic syndrome; pancytopenic condition;
XX myocardial ischaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO9950413-A2.
XX
XX PD 07-OCT-1999.
XX
XX PF 30-MAR-1999; 99WO-US06797.
XX
XX PR 30-MAR-1998; 98US-0079856.
XX PR 20-MAY-1998; 98US-0086074.
XX PR 09-SEP-1998; 98US-0099643.
XX PR 17-DEC-1998; 98US-0112577.
XX PR 18-DEC-1998; 98US-0112703.
XX PR 18-DEC-1998; 98US-0112933.
XX PR 22-DEC-1998; 98US-0113407.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
XX Hui KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
XX Song HY, Wang J, Wu X, Zuckerman SH;
XX WPI: 1999-591319/50.
XX N-PSDB; AA225375.
XX
XX Use of mature FLINT for treating acute liver failure, inflammation,
XX cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
XX and proinflammatory activity
XX
XX Claim 30; Fig 1; 99pp; English.
XX
XX The present invention describes therapeutic applications of mature FLINT
XX (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
XX (mFLINT), which is a member of the tumour necrosis factor receptor
XX superfamily, is used for treating acute liver failure, inflammation of
XX the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
XX with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
XX injury or disorder such as hypercoagulation (including use with
XX thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
XX or disorder, Type I diabetes, cancer, cell damage or damage to an
XX innocent bystander tissue that is induced by a chemotherapeutic agent or
XX therapeutic irradiation, treating haematopoietic progenitor cells that
XX have been exposed to therapeutic radiation or chemotherapy, aplastic
XX anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
XX also used for promoting the growth or differentiation of a haematopoietic
XX progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
XX resulting from abnormal myocardial ischaemia. The present sequence
XX represents human FLINT.
XX
XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.4e-122;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MRALGPGLSLLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQR 60
 Db 1 mraleggpilsllclvlalpallpvpavrgvaetpypwrdaetgerlvcaqcpgpftfvqr 60
 QY 61 PCRRDSPTCGCPPRHYTOFWNYLERCRYCNVLCGEREEERACHATHNRACRGTGFF 120
 Db 61 pcrdrspctcgpcprhytqfwnylerycrncvnlcgerereearachathnrcrctgff 120
 QY 121 AHAGFCLEHASCPGAGVIAPCTPSONTCQPCPGTFSASSSSSEOCOPHRNCTALGLA 180
 Db 121 ahagfclehascpagvgviapctpsntqpcpgtfsasssseocqphrncctalgla 180
 QY 181 LNVPGSSSHDTLTCTSGTGFPLSTRVPGAECERAVIDFVAFQDISIKRLQLLQALEAPE 240
 Db 181 lnpvssshdtlctsgtgfplstrvpgaeeceravidfvafqdisikrlqlqaleape 240
 QY 241 GWGPTPRAGRAALQLKLRRLTELLGAQDGALLVRLQLALVARMPGLERSVRERFLPVH 300
 Db 241 gwgptpragraaalqlklrrltelllgagdgallvrlqlalvarmpglersvrerflpvh 300

RESULT 5

AA17479
 ID AAY17479 standard; Protein; 300 AA.

XX AC AAY17479;

XX DT 02-AUG-1999 (first entry)

XX DE Mammalian tumour necrosis factor receptor OPG-2.

XX KW Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease;
 KW osteopenic disorder; osteoclast activity; primary osteoporosis;
 KW hyperglycaemia; osteolytic metastasis; immune response; cancer.

XX OS Mammalia.

XX PN WO9926977-A1.

XX PD 03-JUN-1999.

XX PF 24-NOV-1998; 98WO-US25065.

XX PR 17-FEB-1998; 98US-0074896.

XX PR 24-NOV-1997; 97US-0066446.

XX PA (BIOJ) BIOGEN INC.

XX PI Tschopp J;

XX DR WPI; 1999-347693/29.

XX DR N-PSDB; AAX76052.

XX PT New tumour necrosis factor family receptor OPG-2

XX PS Claim 1; Page 18; 22pp; English.

XX CC The present sequence represents a mammalian tumour necrosis factor
 CC receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis
 CC factor receptor family, and can be used: (i) to raise specific
 CC antibodies (Ab), (ii) to treat osteopenic disorders associated with
 CC excessive osteoclast activity, e.g. primary osteoporosis, Paget's
 CC disease, hyperglycaemia of malignancy, or osteolytic metastases; (iii)
 CC for affinity purification of cognate ligands, and (iv) to screen for
 CC ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents
 CC such as soluble forms of the protein, are used to prevent, or reduce
 CC severity of, an immune response, and for treating cancer. They can also
 CC be used in diagnostic assays. The nucleic acid sequence encoding OPG-2
 CC can be used as a probe to isolate related sequences from other species.

XX SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALGPGLSLLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQR 60
 Db 1 mraleggpilsllclvlalpallpvpavrgvaetpypwrdaetgerlvcaqcpgpftfvqr 60

QY 61 PCRRDSPTCGCPPRHYTOFWNYLERCRYCNVLCGEREEERACHATHNRACRGTGFF 120
 Db 61 pcrdrspctcgpcprhytqfwnylerycrncvnlcgerereearachathnrcrctgff 120

QY 121 AHAGFCLEHASCPGAGVIAPCTPSONTCQPCPGTFSASSSSSEOCOPHRNCTALGLA 180
 Db 121 ahagfclehascpagvgviapctpsntqpcpgtfsasssseocqphrncctalgla 180

QY 181 LNVPGSSSHDTLTCTSGTGFPLSTRVPGAECERAVIDFVAFQDISIKRLQLLQALEAPE 240
 Db 181 lnpvssshdtlctsgtgfplstrvpgaeeceravidfvafqdisikrlqlqaleape 240

QY 241 GWGPTPRAGRAALQLKLRRLTELLGAQDGALLVRLQLALVARMPGLERSVRERFLPVH 300
 Db 241 gwgptpragraaalqlklrrltelllgagdgallvrlqlalvarmpglersvrerflpvh 300

RESULT 6

AA106817
 ID AAY06817 standard; Protein; 300 AA.

XX AC AAY06817;

XX DT 24-JUN-1999 (first entry)

XX DE Human Dcr3 polypeptide.

XX KW Dcr3 polypeptide; tumour necrosis factor receptor; TNFR; Fas ligand;
 KW apoptosis; T cell mediated immune response; allergy; asthma; cancer;
 KW rheumatoid arthritis; Crohn's disease; guest vs. host disease; human;
 KW gene therapy.

XX OS Homo sapiens.

XX PN WO9914330-A1.

XX PD 25-MAR-1999.

XX PF 18-SEP-1998; 98WO-US19661.

XX PR 30-JUL-1998; 98US-0094640.

XX PR 18-SEP-1997; 97US-0059288.

XX PA (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Botstein D, Dodge KH, Goddard A, Gurney AL;
 PI Kim KJ, Lawrence DA, Pitti R, Roy MA, Tumas DB;
 PI Wood WI;

XX DR WPI; 1999-244032/20.

XX DR N-PSDB; AAX32744.

XX PT Dcr3 polypeptide related to tumor necrosis factor receptor

XX PS Claim 5; Fig 1; 88pp; English.

XX CC This represents a human Dcr3 polypeptide, a homologue of tumour necrosis
 CC factor receptor (TNFR) polypeptide. Host cells containing a vector
 CC comprising the Dcr3 nucleic acid can be used for the recombinant
 CC expression of the protein. Dcr3 binds to Fas ligand, so it (or its
 CC chimeras) are useful for modulating apoptosis in mammalian cells, also
 CC other Fas-ligand induced activities, particularly to inhibit T cell
 CC mediated immune responses, e.g. in treatment of allergy, asthma,
 CC rheumatoid arthritis, Crohn's disease, guest vs. host disease etc. Dcr3

CC may also be used to identify specific binding proteins, potential
 CC inhibitors. Antibodies against Dcr3 are used to treat cancer,
 CC specifically of the lung and colon, also in diagnosis and for affinity
 CC purification of the protein. Detecting mutations in the gene for Dcr3 is
 CC also used to diagnose cancer, or predisposition to it. Dcr3 nucleic acid
 CC is useful as hybridization probe to detect genomic or related sequences;
 CC for chromosome and gene mapping; as source of antisense sequences; for
 CC expression of recombinant Dcr3 and to generate transgenic animals (for
 CC development and screening of therapeutic agents), also for in vivo or
 CC ex vivo gene therapy.

XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPGLSLCLVLALPALLVPVAVRGVAETPTYPWRDAETGERLVCAQCPTGFVQR 60
 DB 1 mralepggisliclvialpallvpavrgvaetptypwrdaetgerlvcaqcpptgfvr 60
 QY 61 PCRRDSPPTTCGPPRRHYTFQWNYLERCRYCNVLCGEREEERACHATHNRACRRTGFF 120
 DB 61 pcrdspttcgpcpprrhytqfwnylerycnvlgereeeearachathnraacrtgff 120
 QY 121 AHAGFCLEHASCPGAGVIAPGTPTSONTCQPCPPTGTFSSSSSEQCQPHRNCRTALGLA 180
 DB 121 ahagfclehascpagviapgtptsontcqpcpptgfsasssseqcqphrncrtalgl 180
 QY 181 LNVPGSSSHDTLTCTGTFPLSTRVPGAECERAVIDFVAFQDISIKRLQRLQALEAPE 240
 DB 181 lnvpgssshdtlctctgfpstrvpgaeceravidfvafqdisikrlqrlqaleape 240
 QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDGLLVRLQALVRMPGLERSVRERFLPVH 300
 DB 241 gwgptpragraalqklrrrltellgaqdgallvrlqalvrmpglersvrerflpvh 300

RESULT 7

AAW97749
 ID AAW97749 standard; Protein; 300 AA.

XX AAW97749;

DT 21-MAY-1999 (first entry)

XX Human tumour necrosis factor receptor ZTNFR-5.

XX ZTNFR-5; tumour necrosis factor receptor; TNFR; human;
 KW cell maturation; bone cell regulation.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..23 /note= "signal peptide"
 FT Protein 24..300 /note= "mature protein"
 FT Domain 24..194 /note= "extracellular domain"
 FT Region 49..71 /note= "cysteine-rich pseudo-repeat 1"
 FT Region 72..113 /note= "cysteine-rich pseudo-repeat 1"
 FT Region 114..151 /note= "cysteine-rich pseudo-repeat 1"
 FT Region 152..194 /note= "cysteine-rich pseudo-repeat 1"

XX WO9904001-A1.

XX 28-JAN-1999.

PD

XX
 PF 21-JUL-1998; 98WO-US15072.
 XX
 PR 21-JUL-1997; 97US-0053203.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Farrah TM;
 DR WPI; 1999-132245/11.
 DR N-PSDB; AAX07226.
 XX
 PT Novel tumour necrosis factor receptor ZTNFR5 - useful for
 PT regulating maturation of TNF-ligand bearing cells
 XX
 PS Claim 1; Page 84-85; 109pp; English.
 XX
 CC This polypeptide comprises a new, secreted tumour necrosis factor
 CC receptor (see AAW97749), designated ZTNFR-5. Novel ZTNFR-5 encoding
 CC polynucleotides and polypeptides were initially identified by
 CC querying an expressed sequence tag (EST) database for sequences
 CC homologous to conserved motifs within the TNF receptor family.
 CC Based on this search, a contig of 16 ESTs (see AAX07226) was
 CC constructed. ZTNFR-5 polypeptides comprise 4 cysteine-rich repeats
 CC (see also AAW97750-55) that are homologous to other TNF receptors, in
 CC particular the soluble, secreted TNF receptor osteoprotegerin.
 CC ZTNFR-5 polypeptide can be prepared by recombinant methods. The
 CC polypeptide, especially the extracellular domain, can be used to
 CC generate a soluble variant of ZTNFR-5. The polypeptides and
 CC nucleic acids can be used to screen for ligands, agonists and
 CC antagonists of ZTNFR-5. The polypeptides can be used in bone cell
 CC regulation and to regulate the maturation of TNF ligand-bearing
 CC cells such as T- or B-cells, lymphocytes, peripheral blood
 CC mononuclear cells, polymorphonuclear leukocytes, fibroblasts or
 CC haematopoietic cells.
 XX
 SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPGLSLCLVLALPALLVPVAVRGVAETPTYPWRDAETGERLVCAQCPTGFVQR 60
 DB 1 mralepggisliclvialpallvpavrgvaetptypwrdaetgerlvcaqcpptgfvr 60
 QY 61 PCRRDSPPTTCGPPRRHYTFQWNYLERCRYCNVLCGEREEERACHATHNRACRRTGFF 120
 DB 61 pcrdspttcgpcpprrhytqfwnylerycnvlgereeeearachathnraacrtgff 120
 QY 121 AHAGFCLEHASCPGAGVIAPGTPTSONTCQPCPPTGTFSSSSSEQCQPHRNCRTALGLA 180
 DB 121 ahagfclehascpagviapgtptsontcqpcpptgfsasssseqcqphrncrtalgl 180
 QY 181 LNVPGSSSHDTLTCTGTFPLSTRVPGAECERAVIDFVAFQDISIKRLQRLQALEAPE 240
 DB 181 lnvpgssshdtlctctgfpstrvpgaeceravidfvafqdisikrlqrlqaleape 240
 QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDGLLVRLQALVRMPGLERSVRERFLPVH 300
 DB 241 gwgptpragraalqklrrrltellgaqdgallvrlqalvrmpglersvrerflpvh 300

RESULT 8

AAW95082
 ID AAW95082 standard; Protein; 300 AA.

XX AAW95082;

XX 20-MAY-1999 (first entry)

DE Orphan receptor (HUMAN NTR-1) polypeptide.

XX HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
 KW tumour necrosis factor receptor; muscle disorder; bone mass; screening;
 KW muscle metabolism; binding agent; cognate ligand.
 XX Homo sapiens.
 OS WO9907738-A2.
 PN 18-FEB-1999.
 PD 04-AUG-1998; 98WO-US16202.
 PF 06-AUG-1997; 97US-0054869.
 PR (PROC) PROCTER & GAMBLE CO.
 PA (REGE-) REGENERON PHARM INC.
 XX Masiakowski PJ, Morris J, Valenzuela DM;
 PI WPI; 1999-167365/14.
 DR N-PSDB; AAX22300.
 XX Novel orphan human receptor polypeptide and nucleic acid - useful as
 PT diagnostic reagents and for treatment of muscle disorders
 PT Claim 7; Page 21; 23pp; English.
 PS This represents a HUMAN NTR-1 polypeptide, a novel orphan receptor. The
 CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor
 CC receptor (TNFR). Host cells transfected with a vector comprising the
 CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the
 CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the
 CC protein are useful for diagnosis and treatment of humans and animals,
 CC especially muscle disorders, as the receptor is involved in regulation of
 CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful
 CC for screening for novel binding agents, and cognate ligands, which may be
 CC used to treat disorders associated with HUMAN NTR-1 imbalance.
 XX Sequence 300 AA:
 SQ
 Query Match 100.0%; Score 1634; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRALGPGLSLCLVLPALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPGTFVQR 60
 DB 1 mraleppglsllclvlpallpvpavrgvaetptyprwdaetgerlvcaqcpptfvqr 60
 QY 61 PCRDSPTTCGPPRRHYTFQWNYLRCRYCNVLCGEREEERACHATHNRACRRTGFF 120
 DB 61 pcrdspttcgpprrhytqfwnylercrycnvlgereeeearachathnrcrctgff 120
 QY 121 AHAGFCLHASCPPGAGVIAPGTPSQNTQCPCPPGTFSASSSSSEQCPHNRCTALGUA 180
 DB 121 ahagfclhascpvgagviapgtpsqntqcpcpggtfsassssseqcqhnrctalgua 180
 QY 181 LNVPGSSSHDTLCTSGTFPLSTRVPGAECERAVIDFVAFODISIKRLORLLQALEAPE 240
 DB 181 lnvpgssshdtlctsgtfplstrvpgaeceravidfvafodisikrlqllqaleape 240
 QY 241 GWGPTPRAGRAALQLKRRRLTELLGADGALLVRLQALVARMPGLERSVRERFLPVH 300
 DB 241 gwgptpragraalqlkrrrltellgagdgallvrlqalvarmpglersvrerflpvh 300
 RESULT 9
 AAB19335
 ID AAB19335 standard; Protein; 300 AA.
 XX
 AC AAB19335;
 XX

DT 19-FEB-2001 (first entry)
 XX A full length human FAS Ligand Inhibitory Protein (FLINT).
 DE Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
 KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
 KW acute respiratory distress syndrome; ulcerative colitis;
 KW chronic obstructive pulmonary disease; Crohn's disease.
 XX Homo sapiens.
 OS WO200038465-A2.
 PN 05-OCT-2000.
 PD 20-MAR-2000; 2000WO-US06417.
 PF 30-MAR-1999; 99US-0126839.
 PR 21-JUN-1999; 99US-0140077.
 PR 21-JUN-1999; 99US-0140156.
 PR 20-OCT-1999; 99US-0160566.
 PR 18-FEB-2000; 2000US-0183398.
 XX (ELIL) LILLY & CO ELI.
 PA Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;
 PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;
 PI Wroblewski VJ;
 XX WPI; 2000-656167/63.
 DR FAS Ligand Inhibitory Protein analogs useful for treating abnormal
 XX apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
 PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's
 PT disease
 XX Disclosure: Page 113-114; 114pp; English.
 PS The present sequence represents a full length human FAS Ligand Inhibitory
 CC protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
 CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
 CC FLINT protein is modified to produce analogues, which have greater
 CC potency, longer in vivo half-lives, decreased aggregation, decreased
 CC absorption onto surfaces, increased solubility and improved ease of
 CC formulation. The FLINT analogue is useful for treating a patient
 CC suffering from disease or condition relating to abnormal apoptosis such
 CC as acute lung injury, acute respiratory distress syndrome, pulmonary
 CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
 CC Crohn's disease.
 XX Sequence 300 AA;
 SQ
 Query Match 100.0%; Score 1634; DB 21; Length 300;
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRALGPGLSLCLVLPALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPGTFVQR 60
 DB 1 mraleppglsllclvlpallpvpavrgvaetptyprwdaetgerlvcaqcpptfvqr 60
 QY 61 PCRDSPTTCGPPRRHYTFQWNYLRCRYCNVLCGEREEERACHATHNRACRRTGFF 120
 DB 61 pcrdspttcgpprrhytqfwnylercrycnvlgereeeearachathnrcrctgff 120
 QY 121 AHAGFCLHASCPPGAGVIAPGTPSQNTQCPCPPGTFSASSSSSEQCPHNRCTALGUA 180
 DB 121 ahagfclhascpvgagviapgtpsqntqcpcpggtfsassssseqcqhnrctalgua 180
 QY 181 LNVPGSSSHDTLCTSGTFPLSTRVPGAECERAVIDFVAFODISIKRLORLLQALEAPE 240
 DB 181 lnvpgssshdtlctsgtfplstrvpgaeceravidfvafodisikrlqllqaleape 240

QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDQALLVRLQLALRVARMPGLSRRERFLPVH 300
Db 241 gwgpctpragraalqklrrrltellgaqdgallvrlqlalrvarmpglsrrerflpvh 300

RESULT 10
AAB28559
ID AAB28559 standard; protein: 300 AA.
XX
AC AAB28559;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human soluble TNF receptor tnfr1-1.
XX
KW Human; tumour necrosis factor like-1; TNF1; tumour necrosis factor; TNF;
KW immunosuppressive; antiarthritic; neuroprotective; dermatological;
KW antinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;
KW colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;
KW osteoporosis; autoimmune disease; myasthenia gravis;
KW insulin-dependent diabetes mellitus.
XX
OS Homo sapiens.
XX
PN WO200060079-A2.
XX
PD 12-OCT-2000.
XX
PF 05-APR-2000; 2000WO-US09058.
XX
PR 05-APR-1999; 99US-0286529.
XX
PA (CHIR) CHIRON CORP.
XX
XX Tribouley C;
PI
DR WPI; 2000-665004/64.
DR N-PSDB; AAC63764.
XX
XX Tumour necrosis factor (TNF) and TNF receptor superfamily protein
PT members TNFR-L and TNFR-L, useful for enhancing or decreasing TNF
PT activities such as inducing cell death and lymphoid organogenesis
XX
PS Claim 1; Page 72; 77pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC human protein designated tumour necrosis factor like-1 (TNFL1). It may be
CC used to induce cell death in tumours, to induce apoptosis of activated T
CC cells, to induce inflammation, and to rescue resting T cells from
CC apoptosis. TNF receptors are used to regulate the function of a TNF
CC ligand which plays a role in apoptosis, inflammation, differentiation, or
CC proliferation. Expression of the receptors can also be useful as markers
CC for cancer, especially for colon cancer. Diseases which can be treated
CC using ligands and/or receptors of the TNF/TNFR superfamily include
CC rheumatoid arthritis, cancer, septic shock, Crohn's disease and
CC osteoporosis. The polynucleotides can be used in gene delivery vehicles,
CC for the purpose of delivering a mRNA or oligonucleotide, full-length
CC protein, fusion protein, polypeptide, or ribozyme, or single-chain
CC antibody, into a cell. The newly identified receptor proteins play
CC regulatory roles in cell proliferation and/or differentiation. The
CC receptors can also play a role in the negative regulation of
CC osteoclastogenesis. Soluble TNFR-like receptors can be useful in the
CC neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be
CC used to treat autoimmune diseases (myasthenia gravis and
CC insulin-dependent diabetes mellitus), tumours, and proliferative
CC disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be
CC delivered to subjects for the purpose of screening test compounds for
CC those which are useful for enhancing transfer of TNF-L subgenomic
CC polynucleotides to the cell or for enhancing subsequent biological
CC effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.4e-122;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALGPGLSLLCLVLALPVPVAVRGVAETPTYPWRDAETGERLVCAQCPPGTFFVOR 60
Db 1 mralepgpplsllclvlalpvpavrgvvaetptypwrdaetgerlvcaqcpptffvqr 60

QY 61 PCRRDSPTTCGPPRHYTFWNLYLERCRYCNVLCGEREEARACHATHNRACRGTGFF 120
Db 61 pcrrdspttcgppprhytqfwnlylercrycnvlgereearachathnracrctgff 120

QY 121 AHAGCFLHASCPGAGVIAPGTSPONTQCPGCTTFSASSSSSQCPHNRCTALGIA 180
Db 121 ahagcflhascpagviapgtspntqcpptffsassysssqcpphnrctalgia 180

QY 181 LNVPGSSSHDTICTCTGFPSTPLSTRVPGAECEERAVDFVAFODISIKRLQLQALEAPE 240
Db 181 lnpvssshdtictctgfpstplstrvpgaeceeravldfvafodisikrlqlqaleape 240

QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDQALLVRLQLALRVARMPGLSRRERFLPVH 300
Db 241 gwgpctpragraalqklrrrltellgaqdgallvrlqlalrvarmpglsrrerflpvh 300

RESULT 11
AAB24057
ID AAB24057 standard; Protein: 300 AA.
XX
AC AAB24057;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO212 protein sequence SEQ ID NO:2.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW nocrotic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytic disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoealic disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US00376.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.
PR 30-NOV-1999; 99WO-US28313.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WT;
XX
XX WPI; 2000-572270/53.
DR N-PSDB; AAC58367.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer -
XX

CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC autoimmune or immune-mediated skin diseases, allergic diseases,
CC immunological diseases of the lung, and transplantation associated
CC diseases including graft rejection and graft-versus-host-disease.
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.4e-122;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPGLSLCLVLALPALLPVPVAVRGVAETPTVPRDAETGERLVCAQCPTGTFVOR 60
DB 1 mralegpglsllclvlalpallpvpavrgvvaetptvprdaetgerlvcaqcpptgfvqr 60
QY 61 PCRRDSPTTCGCPPRHYTFQWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFF 120
DB 61 pccrdspttcgpcprhytfqfwnylercrycnvlgereearachathnracrcrtgff 120
QY 121 AHAGFCLEHASCPPGAGVIAPGTPSONTCQPCPPTGTFSSASSSSSQCPHNRCTALGLA 180
DB 121 ahagfclahasppgagviapgtpsqntgcpcpptgfsasssssqcqhnrctalgla 180
QY 181 LNVPGSSSHDTLCTCTGCPPLSTRVFGAECERAVIDFVAFQDISIKRLQRLQALEAPE 240
DB 181 lnvpgssshdtlctctgfpstrvfgaeceravidfvafqdisikrlqrlqaleape 240
QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDQALLVRLQLALRVARMPGLERSVRERFLPVH 300
DB 241 gwgptpragraalqlkrrrltelgagqgallvrlqlalrvarmpglersvrerflpvh 300

RESULT 13
AAB03621
ID AAB03621 standard; Protein: 300 AA.
XX
AC AAB03621;
XX
DT 03-JAN-2001 (first entry)
XX
DE Human Fas ligand inhibitor FLINT.
XX
KW Human; Fas ligand inhibitor; FLINT: apoptosis; autoimmune disease;
KW inflammation; infectious disease; ischaemia; Alzheimer's disease;
KW Parkinson's disease; Crohn's disease; transplantation.
XX
OS Homo sapiens.

Key Location/Qualifiers
FT Peptide 1..29 /label= signal_peptide
FT Protein 30..300 /label= mature_FLINT
FT Domain 1..42 /label= domain_1
FT Domain 43..85 /label= domain_2
FT Domain 86..122 /label= domain_3
FT Domain 123..165 /label= domain_4
FT

XX WO200034782-A1.
XX 15-JUN-2000.
XX 07-DEC-1999; 99WO-US28696.
XX 09-DEC-1998; 98US-0111575.
XX 09-DEC-1998; 98US-0111580.
XX 07-JAN-1999; 99US-0115069.
XX (ELIL) LILLY & CO ELI.
XX Rosteck PRJ, Song HY, Su EW;
PI WPI; 2000-431379/37.
XX N-PSDB; AAA53208.
XX Novel monkey Fas ligand inhibitor polypeptides, useful for treating
PT inflammatory or autoimmune disease such as rheumatoid arthritis,
PT infectious diseases such as chronic hepatitis, and
PT ischaemia/Re-perfusion conditions -
XX
PS Claim 19; Page 91-93; 101pp; English.
XX
CC The present sequence is the protein sequence of the human Fas ligand
CC inhibitor (FLINT). The FLINT protein is involved in cell-specific
CC apoptosis, and can be used to treat inflammatory and autoimmune diseases
CC such as rheumatoid arthritis, inflammatory bowel disease,
CC graft-versus-host disease, diabetes, psoriasis and Graves' disease,
CC infectious diseases such as HIV-induced lymphopenia, fulminant viral
CC hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
CC ulceration, ischaemia and reperfusion conditions including acute
CC myocardial infarction, acute coronary syndrome, congestive heart failure
CC and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung
CC injury and acute respiratory distress syndrome, Crohn's disease, brain
CC trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic
CC anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and
CC multiple sclerosis. In addition, the protein and its gene can be used to
CC prevent apoptosis following organ transplantation.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.4e-122;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPGLSLCLVLALPALLPVPVAVRGVAETPTVPRDAETGERLVCAQCPTGTFVOR 60
DB 1 mralegpglsllclvlalpallpvpavrgvvaetptvprdaetgerlvcaqcpptgfvqr 60
QY 61 PCRRDSPTTCGCPPRHYTFQWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFF 120
DB 61 pccrdspttcgpcprhytfqfwnylercrycnvlgereearachathnracrcrtgff 120
QY 121 AHAGFCLEHASCPPGAGVIAPGTPSONTCQPCPPTGTFSSASSSSSQCPHNRCTALGLA 180
DB 121 ahagfclahasppgagviapgtpsqntgcpcpptgfsasssssqcqhnrctalgla 180
QY 181 LNVPGSSSHDTLCTCTGCPPLSTRVFGAECERAVIDFVAFQDISIKRLQRLQALEAPE 240
DB 181 lnvpgssshdtlctctgfpstrvfgaeceravidfvafqdisikrlqrlqaleape 240
QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDQALLVRLQLALRVARMPGLERSVRERFLPVH 300
DB 241 gwgptpragraalqlkrrrltelgagqgallvrlqlalrvarmpglersvrerflpvh 300

RESULT 14
AAY97246
ID AAY97246 standard; Protein: 300 AA.
XX

AA97246;
19-DEC-2000 (first entry)
M68 TNF receptor related protein.
M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
receptor; immune response; cell differentiation; ligand; cancer;
bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
Grave's disease; idiopathic myxodema; autoimmune diabetes;
thrombotic thrombocytopenic purpura; multiple sclerosis;
liver diseases; autoimmune gastritis; ulcerative colitis;
glomerulonephritis; pulmonary fibrosis; heart failure;
atherosclerosis; aplastic anaemia; myelodysplastic syndromes;
osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
myocardial infarction; human.
Homo sapiens.
WO200046247-A1.
10-AUG-2000.
04-FEB-2000; 2000WO-US03037.
05-FEB-1999; 99US-0118902.
20-DEC-1999; 99US-0172754.
(MEXI) MERCK & CO INC.
Ba1 C;
WPI; 2000-506066/45.
N-PSDB; AAA53800, AAA53801, AAA53802.
Isolated human M68 nucleic acids and proteins which are part of the
tumour necrosis factor receptor (TNFR) family, useful for identifying
modulators that may be used to treat various diseases e.g. cancer,
osteoporosis, Alzheimer's disease
Claim 1; Page 75-76; 80pp; English.
The M68 protein is a member of a family of proteins which have
roles in immune responses, cell death, cell proliferation and
stimulation of cell differentiation. M68 lacks a transmembrane domain
and is a secreted factor suggesting that it functions as a natural
inhibitor for its ligand. The altered expression pattern of M68 in a
multitude of tissues suggests that M68 may play a role in cancer by
binding to its ligand and blocking apoptotic cell death induced by
such a ligand. This anti-apoptotic role of M68 suggests that
modulators of M68 will be useful in treatment of apoptosis-related
diseases such as various forms of cancer and various bone disorders.
M68 nucleic acids and proteins are therefore useful for treating
conditions involving atypical apoptosis and for identifying
modulators of M68. Modulators of M68 are useful for treatment of
cancer and other diseases associated with abnormal levels of
apoptosis including systemic lupus erythematosus, Hashimoto's
thyroiditis, Grave's disease, idiopathic myxodema, autoimmune
diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
liver diseases, autoimmune gastritis, ulcerative colitis,
glomerulonephritis, pulmonary fibrosis, heart failure,
atherosclerosis, aplastic anaemia, myelodysplastic syndromes,
osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and
myocardial infarction.
Sequence 300 AA;
Query Match 100.0%; Score 1634; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.4e-122;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRALEGPGLSLICLVLPALLPVPVRGVAETPTYPWRDAETGRLVCAQCPPGTFVQR 60

Db 1 mralepglslclclvlalpallpvpavrgvaetptypwrdaetgerlvcaqppgtfvqr 60
QY 61 PCRDRSPPTTCGCPPRHYTFQWNYLRCRYCNVLCGEREEERACHATHNRCRCRTGFF 120
Db 61 pcrdrsppttcgcpprhytqfwnylercrcynvlgereeeearachathnrcrcrtgff 120
QY 121 AHAGFCLHASCPGAGVIAPGTPSONTCQCPPTCTFSASSSSQCPHNRNCTALGLA 180
Db 121 ahagfclhascpagviapgtspqntqccppgtcfassssseqcphnrnctalgla 180
QY 181 LNPVSSSHDTLCTSGTGFPLSTRVPGAECEERAVIDFVAFQDISIKRLQLLALEAPE 240
Db 181 lnpvssshdtlctsgtgfplstrvpgaeceeravidfvafqdisikrlqllqaleape 240
QY 241 GNGPFRAGRAALQKLRRRLTELLCAQDGALLVRLQLALRVARMPGLRSVRERFLPVH 300
Db 241 gngpfragraalqlklrrrltellgaqdgallvrlqlalrvarmpglrsvrerflpvh 300
RESULT 15
AA90357
ID AA90357 standard; Protein; 300 AA.
XX
AC AA90357;
XX
DT 04-DEC-2000 (first entry)
XX
DE Human tumour necrosis factor receptor-6 alpha protein sequence.
XX
KW Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;
KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;
KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;
KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;
KW thyroid associated ophthalmopathy; cell damage; parasitic infection;
KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;
KW neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;
KW psoriasis; septic shock; ulcerative colitis; therapy.
XX
OS Homo sapiens.
XX
PN WO200052028-A1.
XX
PD 08-SEP-2000.
XX
PF 03-MAR-2000; 2000WO-US05686.
XX
PR 04-MAR-1999; 99US-0121774.
PR 12-MAR-1999; 99US-0124092.
PR 27-APR-1999; 99US-0131279.
PR 30-APR-1999; 99US-0131964.
PR 02-AUG-1999; 99US-0146371.
PR 01-DEC-1999; 99US-0168235.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Gentz RL, Ni J, Ebner R, Yu G, Ruben SM, Feng P;
XX
DR WPI; 2000-572174/53.
DR N-PSDB; AAA37772.
XX
PT Nucleic acids encoding human tumour necrosis factor receptor (TNFR)
PT proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.
PT Alzheimer's disease, osteoporosis and graft rejection -
XX
PS Claim 20; Fig 1; 332pp; English.
XX
CC This sequence represents the human tumour necrosis factor receptor 6
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA
CC and protein sequences can be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate TNFR expression. The
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against

CC them may be used for the treatment of a range of conditions such as
CC disorders associated with neovascularisation (especially ocular
CC neovascularisation) (such as solid tumours and malignancies (e.g.
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy
CC and pre-maturity macular degeneration), allergies, inflammation,
CC thyroid associated ophthalmopathy tissue/cell damage, wounds, microbial
CC and parasitic infections, bone disease (e.g. osteoporosis),
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune
CC disorders (e.g. graft rejection), rheumatism, liver disease,
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative
CC colitis.

XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.4e-122;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGSLCLVLALPALLPVPVAVGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 mralepglslclvlalpallpvpavrgvaetptyprdaetgerlvcaqcpptgfvr 60

QY 61 PCRROSPPTTCGPPPHYTQFWNYLERCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 pcrrosppttcgppphytqfwnylercrycnvlgereeeearachathnracrcrtgff 120

QY 121 AHAGFLEHASCPGAGVIAPGTPSONTCQCPGPTFSASSSSSQCPHNRNCTALGLA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 ahagflehscppgagviapgtpsqntcqcpcppgtfsassssseqcphnrnctalgla 180

QY 181 LNVPGSSSHDTLCTSGTGFPLSTRVPGAECEERAVIDFVAFQDISIKRLQRLQALEAPE 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 lnvpgssshdtlctsgtgpplstrvpgaeeceravidfvafqdisikrlqrlqaleape 240

QY 241 GWGPTPRAGRAALQLKRRRLTELLCAQDQGALLVRLQLARVARMPLERSVREPLPVH 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 gwgptpragraalqlkrrrlteillgaqdgallvrlqlarvarmpglersvrerflpvh 300

Search completed: May 10, 2002, 10:53:49
Job time: 78 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:59:02 ; Search time 40.93 Seconds
(without alignments)
968.478 Million cells

Title: US-09-280-567-6
 Perfect score: 1491
 Sequence: 1 VAETPTVPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Dact-nomenclature: Vlakum Vlakub 08

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*

```

1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.mhc:*
8:  sp.organella:*
9:  sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.invertebrate:*
14: sp.unclassified:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1491	100.0	300	4	Q95407	O95407 homo sapien
2	440.5	29.5	372	4	Q9UHP4	Q9UHP4 homo sapien
3	440.5	29.5	401	4	Q00300	Q00300 homo sapien
4	425.5	28.5	401	11	Q08727	O08727 rattus norv
5	424.5	28.5	401	11	Q08712	O08712 mus musculus
6	395	26.5	302	13	Q9PU50	Q9PU50 salvelinus
7	338.5	22.7	425	4	Q16042	Q16042 homo sapien
8	333.5	22.4	459	11	Q62327	Q62327 mus musculus
9	327	21.9	482	11	Q88734	Q88734 mus musculus
10	297	19.9	630	13	Q98SM6	Q98SM6 gallus gall
11	288.5	19.3	655	11	Q9EPU5	Q9EPU5 mus musculus
12	287	19.2	655	4	Q75509	Q75509 homo sapien
13	275	18.4	348	12	Q57277	Q57277 monkeypox v
14	275	18.4	348	12	Q57103	Q57103 monkeypox v
15	275	18.4	348	12	Q57108	Q57108 monkeypox v
16	270.5	18.1	349	12	Q57100	Q57100 monkeypox v
17	268.5	18.0	349	12	Q57291	Q57291 monkeypox v
18	268.5	18.0	349	12	Q57101	Q57101 monkeypox v
19	268.5	18.0	349	12	Q57102	Q57102 monkeypox v

20	267.5	17.9	349	12	057099	057099	monkeypox v
21	260	17.4	348	12	057112	057112	variola vir
22	260	17.4	348	12	057112	057112	variola vir
23	260	17.4	349	12	057110	057110	variola vir
24	260	17.4	349	12	057110	057110	variola vir
25	260	17.4	349	12	057110	057110	variola vir
26	260	17.4	349	12	057110	057110	variola vir
27	260	17.4	349	12	057110	057110	variola vir
28	259	17.4	360	12	057118	057118	cowpox viru
29	258.5	17.3	355	12	057308	057308	cowpox viru
30	257.5	17.3	326	12	057120	057120	cowpox viru
31	257.5	17.3	349	12	057284	057284	camelpox v1
32	257.5	17.3	349	12	057098	057098	camelpox v1
33	254.5	17.1	326	12	057122	057122	cowpox viru
34	254.5	17.1	351	12	073559	073559	cowpox viru
35	253.5	17.0	349	12	057305	057305	cowpox viru
36	253.5	17.0	349	12	057097	057097	camelpox v1
37	253.5	17.0	351	12	057117	057117	cowpox viru
38	252	16.9	349	12	057109	057109	variola vir
39	251	16.8	347	12	057119	057119	cowpox viru
40	249.5	16.7	347	12	057115	057115	cowpox viru
41	248.5	16.7	351	12	057121	057121	cowpox viru
42	245.5	16.5	350	12	057123	057123	cowpox viru
43	244	16.4	283	6	Q9XSZ8	Q9XSZ8	cercopithec
44	235.5	15.8	616	4	Q9Y6Q6	Q9Y6Q6	homo sapien
45	230.5	15.5	276	13	Q9DD62	Q9DD62	gallus gall

ALIGNMENTS

RESULT	1	
ID	095407	PRELIMINARY; PRT; 300 AA.
AC	095407;	
DT	01-MAY-1999	(TEMBLrel. 10, Created)
DT	01-MAY-1999	(TEMBLrel. 10, Last sequence update)
DT	01-JUN-2001	(TEMBLrel. 17, Last annotation update)
DE	DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1).	
GN	DCR3 OR TR6 OR TNFRSF6B.	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RI	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE-99087326; PubMed-9872321;	
RA	Pittl R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,	
RA	Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,	
RA	Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,	
RA	Goddard A.D., Botstein D., Ashkenazi A.;	
RT	"Genomic amplification of a decoy receptor for Fas ligand in lung and	
RT	colon cancer.";	
RL	Nature 396:699-703(1998).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=BLOOD;	
RX	MEDLINE-99253915; PubMed-10318773;	
RA	Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;	
RT	"A newly identified member of tumor necrosis factor receptor	
RT	superfamily (TR6) suppresses LIGHT-mediated apoptosis.";	
RT	J. Biol. Chem. 274:13733-13736(1999).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=PANCREAS;	
RX	MEDLINE-20122600; PubMed-10655513;	
RA	Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,	
RA	Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;	
RT	"Overexpression of M68/DCR3 in human gastrointestinal tract tumors	
RT	Independent of gene amplification and its location in a four-gene	
RT	cluster.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).	
RN	[4]	

SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF104419; AAD03056.1; -;
DR EMBL: AF134240; AAD29688.1; -;
DR EMBL: AF217796; AAF35244.1; -;
DR EMBL: AF217793; AAF33685.1; -;
DR EMBL: AF217794; AAF33686.1; -;
DR EMBL: AL121845; CAC03668.1; -;
DR HSP: P25942; ICDP.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS01186; EGF 2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR.1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR.2; 2.
KW Receptor.
SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;

Query Match 100.0%; Score 1491; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.5e-126;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDPTTCGPPRHYTQFWNYLERCR 60
DB 30 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDPTTCGPPRHYTQFWNYLERCR 89
QY 61 YCNVLGGEREEARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTQ 120
DB 90 YCNVLGGEREEARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTQ 149
QY 121 COPCPGTTSSASSSQCPQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 180
DB 150 COPCPGTTSSASSSQCPQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 209
QY 181 ECERAVIDEFAVDISIKRLRLQLALEAPGPGTPPRAGRAALQLKLRRLTELLGAQD 240
DB 210 ECERAVIDEFAVDISIKRLRLQLALEAPGPGTPPRAGRAALQLKLRRLTELLGAQD 269
QY 241 GALLVRLQLALVARMPGLSVRSRFLPVH 271
DB 270 GALLVRLQLALVARMPGLSVRSRFLPVH 300

RESULT 2
Q9UHP4 PRELIMINARY; PRT; 372 AA.
AC Q9UHP4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL: AF134187; AAF20168.1; -;
DR HSP: P25942; ICDP.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 4.

DR PROSITE: PS00652; TNFR_NGFR.1; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 29.5%; Score 440.5; DB 4; Length 372;
Best Local Similarity 41.2%; Pred. No. 1e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYPWRDAETGERLVCAQCPGTFVQPCRRDPTTCGPPRHYTQFWNYLERCRVCNV 64
DB 5 PKYLHYDEETSQHLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECLYCS 64
QY 65 LCGEREEARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTQCP 124
DB 65 VCRELYVVKQECNTHNRVCECKEGRYLETEFLKHKRSCPPGFGVQAGTPERTVCKRC 124
QY 125 PGCTFSASSSQCPQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAEE--C 182
DB 125 PDGFFSNETSSKAPCRKHTNCSVFGLLTQKGNATHDNI---CSGSESTQKCGIDVTLC 181
QY 183 ERAVIDF 189
DB 182 ERAFFRF 188

RESULT 3
O00300 PRELIMINARY; PRT; 401 AA.
AC O00300; O60236;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPF OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trall G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RA MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trall G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density";
RL Cell 89:309-319(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor";
RL Eur. J. Biochem. 254:685-691(1998).

CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
 CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
 CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
 CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL; AB002146; BAA25910.1; -.
 CC EMBL; AB008822; BAA32076.1; -.
 CC EMBL; AB008821; BAA32076.1; JOINED.
 CC EMBL; U94332; AAB53709.1; -.
 CC HSP; P25942; ICDF.
 CC MIM: 602643; -.
 CC InterPro; IPR000488; Death.
 CC InterPro; IPR001368; TNFR_c6.
 CC Pfam; PF00020; TNFR_c6; 3.
 CC ProDom; PD000771; TNFR_c6; 1.
 CC SMART; SM00005; DEATH; 1.
 CC SMART; SM00208; TNFR; 4.
 CC PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 CC PROSITE; PS00500; TNFR_NGFR_2; 2.
 CC Glycoprotein; Repeat; Cytokine; Signal.
 CC SIGNAL 1 21 BY SIMILARITY.
 CC CHAIN 22 401 OSTEOPROTEGERIN.
 CC DOMAIN 23 63 4 X TNFR-CYS.
 CC REPEAT 23 63
 CC REPEAT 107 143 TNFR-CYS 1.
 CC REPEAT 144 201 TNFR-CYS 2.
 CC REPEAT 144 201 TNFR-CYS 3.
 CC REPEAT 144 201 TNFR-CYS 4.
 CC DOMAIN 306 365 DEATH DOMAIN.
 CC DISULFID 41 54 BY SIMILARITY.
 CC DISULFID 44 62 BY SIMILARITY.
 CC DISULFID 65 80 BY SIMILARITY.
 CC DISULFID 83 97 BY SIMILARITY.
 CC DISULFID 87 105 BY SIMILARITY.
 CC DISULFID 118 142 BY SIMILARITY.
 CC DISULFID 145 160 BY SIMILARITY.
 CC CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
 CC SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;
 Query Match 29.5%; Score 440.5; DB 4; Length 401;
 Best Local Similarity 41.2%; Pred. No. 1.1e-31;
 Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;
 QY 5 PYPWDAETGERLVCACQPGTFVORPCRRDSTTCGCPPHRYTQFNLYLRCYCNV 64
 DB 26 PKYLHYDEETSHQLLCKCPGPGTYLKQHTAKWKTKAPCPDHYTDSWHTSDECLYCSP 85
 QY 65 LCGEREERACHATHNACRRTGFFAHAGFCLEHASCPGAGVIAPGTPSONTOCOPC 124
 DB 86 VKELQYVQECNRTNHNVCEKEGYLEIEFCLKRRSCPPGFGVVOAGPERRNTVKRC 145
 QY 125 PGCTFSASSSSSQCPHRNCTALGALNVPGSSSHDTLCTCTGTFPLSTRVPGABE--C 182
 DB 146 PDGFFSNETSSRACPKRHTNCVSFGLLLQTKGNATHDNI---CSGNSESTQKCIDVTLC 202
 QY 183 ERAVIDF 189
 DB 203 EEAFFRF 209

RESULT 4
 O08727 ID O08727 PRELIMINARY; PRT; 401 AA.
 AC O08727;
 DT 01-JUL-1997 (T-EMBLrel. 04, Created)
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).
 GN TNFRSF11B OR OPG.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_Taxid=101116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation
 of bone density.";
 RL Cell 89:309-319(1997).
 CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL; U94330; AAB53707.1; -.
 CC HSP; P25942; ICDF.
 CC InterPro; IPR000488; Death.
 CC InterPro; IPR001368; TNFR_c6.
 CC Pfam; PF00020; TNFR_c6; 4.
 CC ProDom; PD000771; TNFR_c6; 1.
 CC SMART; SM00005; DEATH; 1.
 CC SMART; SM00208; TNFR; 4.
 CC PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 CC PROSITE; PS00500; TNFR_NGFR_2; 2.
 CC Glycoprotein; Repeat; Cytokine; Signal.
 CC SIGNAL 1 21 BY SIMILARITY.
 CC CHAIN 22 401 OSTEOPROTEGERIN.
 CC DOMAIN 23 201 4 X TNFR-CYS.
 CC REPEAT 23 63
 CC REPEAT 64 106 TNFR-CYS 1.
 CC REPEAT 107 143 TNFR-CYS 2.
 CC REPEAT 144 201 TNFR-CYS 3.
 CC REPEAT 144 201 TNFR-CYS 4.
 CC DOMAIN 306 365 DEATH DOMAIN.
 CC DISULFID 41 54 BY SIMILARITY.
 CC DISULFID 44 62 BY SIMILARITY.
 CC DISULFID 65 80 BY SIMILARITY.
 CC DISULFID 83 97 BY SIMILARITY.
 CC DISULFID 87 105 BY SIMILARITY.
 CC DISULFID 118 142 BY SIMILARITY.
 CC DISULFID 145 160 BY SIMILARITY.
 CC CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 401 AA; 46192 MW; FEC6A31FD4E573A CRC64;
 Query Match 28.5%; Score 425.5; DB 11; Length 401;
 Best Local Similarity 39.5%; Pred. No. 2.5e-30;
 Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;

QY 5 PTPWRDAETGERLVCAQCPPTGFVQPCRRDSTTCGCPGPPRHRYTQFWNYLRCRYCNV 64
 DB 26 PKYLHYDPETGTHLLCDKCAPGYLKHQCTVRKTLCLVPCPDYSDTDSWHTSDCYVCS 85
 QY 65 LCGEREEARACHATINRACRGTGFFAHAGFCLHSCPPGAGVAPGTPSNTQOCPC 124
 DB 86 VKELQTVQECNRTNVRVCEBEGRYLEFELCKHRSCPPGLGVQAGTPERTVCKRC 145
 QY 125 PPGTFSSASSSSQCPHRCNCTALGLALNVPGSSSHDTLCTCTGTFPLSTRVPCAEE--C 182
 DB 146 PDGFFSGTSSKAPCRKHTNCSSLSGLLLIQKNATHDNV---CSGNREATQNGIDVTL 202
 QY 183 ERAVIDFAFQDISIKRLQRLQAL 207
 DB 203 EEAFFRFAVPTKIIPNWSLVVDLSL 227

RESULT 5
 O08712 PRELIMINARY; PRT; 401 AA.

AC O08712; O70202;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).
 DE (OCIF).
 GN TNFRSF11B OR OPG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=KIDNEY;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Luehly R., Nguyen H.O., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.";
 RL Cell 89:309-319(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/OLA. AND NIH SWISS;
 RX MEDLINE=98382527; PubMed=9714833;
 RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
 RA Higashio K.;
 RA "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
 RT gene and its expression in embryogenesis.";
 RL Gene 215:339-343(1998).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
 CC PLACENTA. NOT DETECTED IN SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
 CC 15 TO DAY 17.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; U94331; AAB53708.1; -;
 DR EMBL; AB013898; BAA28269.1; -;
 DR EMBL; AB013903; BAA33388.1; -;
 DR EMBL; AB013899; BAA33388.1; JOINED.
 DR EMBL; AB013900; BAA33388.1; JOINED.
 DR EMBL; AB013901; BAA33388.1; JOINED.

DR EMBL; AB013902; BAA33388.1; JOINED.
 DR HSSP; P25942; ICDF.
 DR MGD; MGI:109587; Tnftrsf11b.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00017; DEATH_DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00652; TNFR_NGFR_2; 2.
 KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21 OSTEOPROTEGERIN.
 FT CHAIN 22 401 4 X TNFR-CYS.
 FT DOMAIN 23 201 TNFR-CYS 1.
 FT REPEAT 23 63 TNFR-CYS 2.
 FT REPEAT 64 106 TNFR-CYS 3.
 FT REPEAT 107 143 TNFR-CYS 4.
 FT REPEAT 144 201 DEATH DOMAIN.
 FT DOMAIN 306 365 BY SIMILARITY.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH SWISS).
 FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).
 FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).
 FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).
 FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).
 FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 28.5%; Score 424.5; DB 11; Length 401;
 Best Local Similarity 39.0%; Pred. No. 3e-30;
 Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;

QY 5 PTPWRDAETGERLVCAQCPPTGFVQPCRRDSTTCGCPGPPRHRYTQFWNYLRCRYCNV 64
 DB 26 PKYLHYDPETGTHLLCDKCAPGYLKHQCTVRKTLCLVPCPDYSDTDSWHTSDCYVCS 85
 QY 65 LCGEREEARACHATINRACRGTGFFAHAGFCLHSCPPGAGVAPGTPSNTQOCPC 124
 DB 86 VKELQTVQECNRTNVRVCEBEGRYLEFELCKHRSCPPGLGVQAGTPERTVCKRC 145
 QY 125 PPGTFSSASSSSQCPHRCNCTALGLALNVPGSSSHDTLCTCTGTFPLSTRVPCAEE--C 182
 DB 146 PDGFFSGTSSKAPCRKHTNCSSLSGLLLIQKNATHDNV---CSGNREATQNGIDVTL 202
 QY 183 ERAVIDFAFQDISIKRLQRLQAL 207
 DB 203 EEAFFRFAVPTKIIPNWSLVVDLSL 227

RESULT 6
 Q9PUS0 PRELIMINARY; PRT; 302 AA.
 ID Q9PUS0
 AC Q9PUS0
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

```
DE DECOY RECEPTOR.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor receptor homolog is up-regulated in the brook
RL trout (Salvelinus fontinalis) ovary at the completion of ovulation.";
DR EMBL: AF156738; AAD56428.1; -.
DR HSSP: P19438; IEXT.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 26.5%; Score 395; DB 13; Length 302;
Best Local Similarity 34.3%; Pred. No. 1e-27;
Matches 82; Conservative 44; Mismatches 101; Indels 12; Gaps 7;

QY 6 TYPWRDAETGERLVACQPGTFFORCRDSTTCGCPGPRHYTQFWNYLERCRYCNVL 65
DB 22 TFNDDRYSGLSVCDRCPPGTLYLRAPCSAMRKSDCACPNGAYTEFWNHISKLRCS-M 80
QY 66 CGEREPEARACHATHRACRCRTGFFAHAGF--CLEHASCPPGAGVIAPGTPSQTQCP 123
DB 81 CAENOVVKQECSPNSNCECKEGYFNKKYEACIKHKCPGGVANTGTGPHDTECVQ 140
QY 124 CPGTFSASSSSQOPHNCRTALGLALNVPSSSDHTLTCTSGTGPLSTRVPGAEECE 183
DB 141 COAGFSEVSATCATCQAQSNCKYGVVVLKGDWHNTLCASC--YDLKTR-DGAEYLH 197
QY 184 RAVIDEV--AFODISIKRLQRLQALEAPEGSGWPTPRAGRAALQKLRRRLTELLGAOD 240
DB 198 EILPTFIIQLHQTGIRMRRL--AMRLPQGGKKPLIG--AVMKRNRRGLHDFMNSWD 252

RESULT 7
ID Q16042 PRELIMINARY; PRT; 425 AA.
AC Q16042;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytokine 2:231-237(1990).
DR EMBL: S83368; AAB19824.2; -.
DR HSSP: P25942; ICDF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 4.

Query Match 22.4%; Score 333.5; DB 11; Length 459;
Best Local Similarity 29.7%; Pred. No. 5e-22;
Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;
```

```
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 425 AA; 44608 MW; 1B24A97E3AD4CF9F CRC64;

Query Match 22.7%; Score 338.5; DB 4; Length 425;
Best Local Similarity 30.1%; Pred. No. 1.7e-22;
Matches 82; Conservative 43; Mismatches 110; Indels 37; Gaps 9;

QY 17 RLVCAQCPGPGTFFORCRDSTTCGCPGPRHYTQFWNYLERCRYCNVLGGEREEARAC 76
DB 15 QMCCSKCSPGQAHKVFCTKTSDTVDCSDCEDSTYTQLMWNVPECLSGRCSSDQVETQAC 74
QY 77 HATHRACRCRTGFFAHAGF-----FCLHASCPPGAGVIAPGTPSQTQCPGPGTFS 130
DB 75 TREQNRICTCRPGWYCALSKOEGCRLCAPLRKCRPGFVARPGTETSDVCKPCAPGTF 134
QY 131 ASSSSQOCQPHNCRNTALGLALNVPSSSDHTLTCTSGTGPLSTRVPGAEECERAVIDFV 190
DB 135 NTSSTDICRPHQICNVVA----IPGNASMDAVCTST--PTRSMAPGAVHLPQVPV---- 184
QY 191 AFODISIKRLQRLQALEAPE-----GSGTPRA----GRAALQKLRRRLTELLGAODG 241
DB 185 ---STRQHTQTPSTAPSTSTSLPMPGPPAGSGTGDFALPVGLIVGTAL-----G 236
QY 242 ALLVRLQLAL---RVARMP-GLERSVRERFLP 269
DB 237 LLIGVNVVIMTQVKKKPLCLQREAKVPHLP 268

RESULT 8
ID Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD;
RA MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL: X76401; CAA53981.1; -.
DR HSSP: P19438; INCF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
FT NON_TER 1
FT VARIANT 87 87 S->T.
FT VARIANT 93 93 T->I.
FT VARIANT 268 268 F->I.
FT VARIANT 345 345 S->F.
FT VARIANT 421 421 Y->C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 22.4%; Score 333.5; DB 11; Length 459;
Best Local Similarity 29.7%; Pred. No. 5e-22;
Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;
```

```
QY 17 RLVCACPPCTFVQPCRRDPTTCGCPRRHYTFQWNYLRCRYCNVLCGEREAC 76
Db 37 QMCCAKCPGGQYVKHFCNKTSDTVACDEASMTVMNQFRTCLSCSSCSTQVETRAC 96
QY 77 HATHNRACRGTGFF-----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCPCPGTF 129
Db 97 TKOONRVACEAGRYCALKTHSGRCMRLSKGPGFGVASSRAPNGNVLKACAPGTF 156
QY 130 SASSSSEOCQPHNCTALGNVPGSSSHDTLCT---SCTGFPLSTRVPGAEECERA 185
Db 157 SDTSSDVCPRHRICSILA---IPGNASTDAVCAPESTLSAIPRTLVSQPEPTRSQ 212
QY 186 VIDFVAPQDISIKRLQRLQALFAPEGWPTP-----RAGRAALQLKRLRLTELLGAQD 240
Db 213 PLD-----QEPGSPQTSILTSL-----GSTPIEQSTKGISLPIGLIVGVTSL----- 257
QY 241 GALLVRLQLAL-----RVARNPGLSRRERFLP 269
Db 258 GLLMLGLVNCFILVQRKKPKSCLQORDAKVPHVP 290

RESULT 9
O88734 PRELIMINARY; PRT; 482 AA.
AC Q88734;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
BT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE P80 TNF-ALPHA RECEPTOR.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor Gene: Genomic Structure and
RT Characterization of the two Transcripts.";
RL Genomics 0:0-0(0).
DR EMBL; Y14619; CAAT4969.1;
DR EMBL; Y14620; CAAT4969.1; JOINED.
DR EMBL; Y14621; CAAT4969.1; JOINED.
DR EMBL; Y14622; CAAT4969.1; JOINED.
DR EMBL; Y14623; CAAT4969.1; JOINED.
DR EMBL; Y14679; CAAT4969.1; JOINED.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS0050; TNFR_NGFR_2; 3.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FFB3C CRC64;

Query Match 21.9%; Score 327; DB 11; Length 482;
Best Local Similarity 29.3%; Pred. No. 2e-21;
Matches 82; Conservative 43; Mismatches 109; Indels 46; Gaps 10;

QY 17 RLVCACPPCTFVQPCRR-----DSPTTCGCPRRHYTFQWNYLRCRYCNVLCGER 69
Db 52 QMCCAKCPGGQYVKHFCNKTSDTVACADSDTVCADEASMTVMNQFRTCLSCSSCSTD 111
QY 70 EEARACHATHNRACRGTGFF-----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQ 122
Db 112 QVETRACRKOONRVACEAGRYCALKTHSGRCQRCQRLSKCGFGFVASSRAPNGNVLCK 171
QY 123 PCPPGTFSSASSSSQCPHNRCTALGNVPGSSSHDTLCT-----SCTGFPLSTRVPG 178
Db 172 ACAPGTFSDTSDTVCRPHRISILA----IPGNASTDAVCAPESTLSAIPRTLVSQ 227
QY 179 AEECERAVIDFVAFQDISIKRLQRLQALFAPEGWPTP-----RAGRAALQLKRLRLT 233
```

```
Db 228 PEPTRSQPLD-----QEPGSPQTSILTSL-----GSTPIEQSTKGISLPIGLIVGT 277
QY 234 ELLGAQDQALVRLQLAL-----RVARNPGLSRRERFLP 269
Db 278 SL-----GLLMLGLVNCFILVQRKKPKSCLQORDAKVPHVP 312

RESULT 10
Q98SM6 PRELIMINARY; PRT; 630 AA.
AC Q98SM6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DEATH RECEPTOR 6 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349908; AAK29666.1;
KW Receptor.
FT NON_TER.
SQ SEQUENCE 630 AA; 68977 MW; 53C53BD1C4B25567 CRC64;

Query Match 19.9%; Score 297; DB 13; Length 630;
Best Local Similarity 34.2%; Pred. No. 1.3e-18;
Matches 55; Conservative 27; Mismatches 79; Indels 0; Gaps 0;

QY 11 DAETGERLVCACPPGTFVQPCRRDPTTCGCPRRHYTFQWNYLRCRYCNVLCGERE 70
Db 22 DRATNELICDKCPAGTVVSKHCTKTLRECSPCPDGTFTHKENGIERCHPCRPCLPM 81
QY 71 EEARACHATHNRACRGTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQCPCPGTF 130
Db 82 IEKTHCTALTDRCTCLSGTFQINDTCVPTVCPGVGVRKKGTETEDVRCKPCPGTF 141
QY 131 ASSSSSEOCQPHNCTALGNVPGSSSHDTLCTSCGTP 171
Db 142 DVPSSVMKCKTYTDCFGKNVYVYKPKESDNVCGSPASLP 182

RESULT 11
Q98PU5 PRELIMINARY; PRT; 655 AA.
AC Q98PU5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=KIDNEY;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT (DR6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF322069; AAG38115.1;
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:59:24 ; Search time 15.03 Seconds
(without alignments)
661.089 Million cell updates/sec

Title: US-09-280-567-6
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVAMPGLERSVRERFLPVH 271

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342.5	23.0	461	1	TNR2_HUMAN
2	332.5	22.3	474	1	TNR2_MOUSE
3	299.5	20.1	435	1	TNR2_HUMAN
4	265.5	17.8	415	1	TNR2_MOUSE
5	260	17.4	349	1	VC22_VARV
6	244	16.4	283	1	TR14_HUMAN
7	234.5	15.7	325	1	VT2_SFVKA
8	215.5	14.5	277	1	OX40_HUMAN
9	211.5	14.2	271	1	OX40_RAT
10	211	14.2	277	1	CD40_HUMAN
11	210.5	14.1	326	1	VT2_MTXVL
12	203	13.6	289	1	CD40_MOUSE
13	202	13.5	269	1	CD40_BOVIN
14	194.5	13.0	272	1	OX40_MOUSE
15	185	12.4	256	1	41BB_MOUSE
16	182	12.2	595	1	CD30_HUMAN
17	174	11.7	255	1	41BB_HUMAN
18	171.5	11.5	416	1	NGFR_CHICK
19	168	11.3	425	1	NGFR_RAT
20	163	10.9	332	1	FASA_PIG
21	158	10.6	427	1	NGFR_HUMAN
22	155.5	10.4	327	1	FASA_MOUSE
23	155	10.4	323	1	FASA_BOVIN
24	153	10.3	241	1	TR18_HUMAN
25	148	9.9	250	1	CD27_MOUSE
26	147.5	9.9	5376	1	ZAN_MOUSE
27	145	9.7	335	1	FASA_HUMAN
28	143.5	9.6	471	1	TNR1_BOVIN
29	142.5	9.6	260	1	CD27_HUMAN
30	137.5	9.2	324	1	FASA_RAT
31	130.5	8.8	454	1	TNR1_MOUSE
32	128.5	8.6	417	1	WSL1_HUMAN
33	128.5	8.6	3635	1	LMA5_MOUSE

34	127	8.5	1192	1	LMG2_MOUSE	Q61092	mus musculus
35	125.5	8.4	1877	1	PKC5_MOUSE	Q04592	mus musculus
36	124.5	8.4	1696	1	PKC5_BRACL	Q9nj15	branchiosto
37	124.5	8.4	1713	1	LMA3_HUMAN	Q16787	homo sapien
38	123.5	8.3	455	1	TNR1_HUMAN	P19438	homo sapien
39	123	8.2	2569	1	LMA3_MOUSE	Q61789	mus musculus
40	121	8.1	3106	1	LMA2_MOUSE	Q60675	mus musculus
41	120	8.0	1609	1	LMG1_HUMAN	P11047	homo sapien
42	119.5	8.0	3084	1	LMA1_MOUSE	P19137	mus musculus
43	118.5	7.9	461	1	TNR1_RAT	P22934	rattus norv
44	118.5	7.9	1680	1	FUR2_DROME	P30432	drosophila
45	118	7.9	913	1	PKC5_HUMAN	Q92824	homo sapien

ALIGNMENTS

RESULT	1
TNR2_HUMAN	
ID	TNR2_HUMAN
AC	P20333;
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBP11) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
GN	TNFRSF1B OR TNFR2 OR TNFR.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=90260639; PubMed=2160731;
RA	Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.;
RA	"A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";
RT	Cellular and viral proteins.";
RL	Science 248:1019-1023(1990).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91045991; PubMed=2172983;
RA	Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT	"A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96299745; PubMed=8661109;
RA	Beltlinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J., Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J., Brodeur G.M.;
RT	"Physical mapping and genomic structure of the human TNFR2 gene.";
RL	Genomics 35:94-100(1996).
RN	[4]
RP	SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX	MEDLINE=90349572; PubMed=2166946;
RA	Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;
RT	"Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN	[5]
RP	SEQUENCE OF 27-31.
RX	MEDLINE=90110215; PubMed=2153136;
RA	Engelmann H., Novick D., Wallach D.;
RT	"Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";
RL	J. Biol. Chem. 265:1531-1536(1990).
RN	[6]
RP	SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.

RT necrosis factor receptors demonstrate one receptor is species
 RT specific.", Acad. Sci. U.S.A. 88:2830-2834(1991).
 RL [2]

RN SEQUENCE FROM N.A.
 RX MEDLINE=91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor,"
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]

RN SEQUENCE OF 1-26 FROM N.A.
 RC STRAIN=NOD;
 RC Jacob C.O., Liu J.;

RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]

RN SEQUENCE OF 1-22 FROM N.A.
 RC TISSUE=Liver;

RA Kissnerghis M., Fellows R., Feldmann M., Chernajovsky Y.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; M60459; AAA39752.1; -;
 DR EMBL; M59378; AAA40463.1; -;
 DR EMBL; U39488; AAA85021.1; -;

DR EMBL; X87128; CAA60618.1; -;
 DR PIR; B38634; B38634.

DR HSP; P19438; INCF.

DR MGD; MGI:1314883; Tnfrsf1b.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 4.

DR ProDom; PD000771; TNFR_c6; 1.

DR SMART; SM00208; TNFR; 4

DR PROSITE; PS00852; TNFR_NGFR_1; 2.

DR PROSITE; PS00500; TNFR_NGFR_2; 3.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 22

FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.

FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 259 288 POTENTIAL.

FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 39 203 4 X TNFR-CYS.

FT REPEAT 39 77 TNFR-CYS 1.

FT REPEAT 78 119 TNFR-CYS 2.

FT REPEAT 120 164 TNFR-CYS 3.

FT REPEAT 165 203 TNFR-CYS 4.

FT DISULFID 40 54 BY SIMILARITY.

FT DISULFID 55 68 BY SIMILARITY.

FT DISULFID 58 76 BY SIMILARITY.

FT DISULFID 79 94 BY SIMILARITY.

FT DISULFID 97 111 BY SIMILARITY.

FT DISULFID 101 119 BY SIMILARITY.

FT DISULFID 121 127 BY SIMILARITY.

FT DISULFID 136 145 BY SIMILARITY.

FT DISULFID 139 163 BY SIMILARITY.

FT DISULFID 166 181 BY SIMILARITY.

FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match

22.3%; Score 332.5; DB 1; Length 474;

Best Local Similarity 29.7%; Pred. No. 2.le-19;
 Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

QY 17 RLVCACQPGTFTVQPCRRDSTTCGPPRHYTQFWNYLERCYNVLCGEREEARAC 76
 : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : |||||
 Db 52 QMCCAKCPGQVVKHFCNKTSITVDCADCEASMYTQWVQNFRTCLSCSSCTTQDVEIRAC 111
 : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : |||||
 QY 77 HATHNRACRRTGFF-----AHAGF---CLEHASCPPGAGVIAGTPTSONTCQCPGTF 129
 : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : |||||
 Db 112 TKQNRVCAACEAGRYCALKTHSGCRQKRLSKGFGFVASSRANGNVLCACAPGTF 171
 : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : |||||
 QY 130 SASSSSEOCQPHRNCTALGLALNVPGSSSHDTLCT-----SCTGFPLSTRVPGAECCERA 185
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||
 Db 172 SDTTSSTDVCRPHRICSI-----IFGNASTDAVCAPESTLSAIPRTLYVSQPEPTRSQ 227
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||
 QY 186 VIDFAVQDISIKRLQRLQALAEPEGWGP-----RAGRAALQKLRRRLTELIGAQD 240
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||
 Db 228 PLD-----QEPGPSQTSILTS-----GSTPIEQSTKGGISLPIGLIVGVTSL----- 272
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||
 QY 241 GALLVRLQAL-----RVARMPLGLSVRERFLP 269
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||
 Db 273 GLLMGLVNCIILVQRKKKPSCLQRDAKVPHP 305
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||

RESULT 3

ID TNRC_HUMAN STANDARD; PRT; 435 AA.
 AC P36941;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
 DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
 GN LTBR OR TNFR OR TNFRSF3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93252381; PubMed=8486360;
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;

RT "Construction and evaluation of a hncDNA library of human 12p
 RT transcribed sequences derived from a somatic cell hybrid.";
 RL Genomics 16:214-218(1993).
 RN [2]

RN FUNCTION.

RX MEDLINE=94225209; PubMed=8171323;

RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.;

RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;

RT "A lymphotoxin-beta-specific receptor.";

RL Science 264:707-710(1994).

CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 CC IMMUNE DEVELOPMENT.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; L04270; AAA36757.1; -;

DR HSP; P25942; ICDF.

DR MIM; 600979; -;

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 4.

DR ProDom; PD000771; TNFR_c6; 1.

DR SMART; SM00208; TNFR; 4.

```

DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR RECEPTOR; PS00500; TNFR_NGFR_2; 3.
KW SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.
FT DOMAIN 228 248 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 249 435 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 211 4 X TNFR-CYS.
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 624626E5022F656F CRC64;

Query Match 20.1%; Score 299.5; DB 1; Length 435;
Best Local Similarity 32.0%; Pred. No. 7.8e-17;
Matches 74; Conservative 27; Mismatches 101; Indels 29; Gaps 9;

QY 13 ETGERLVCAQCPGTFVQRCRDSPTTCGPPRHYTFQWNYL---ERCRCYNVLCGER 69
DB 52 EPQHRICCSRCPTGYVSAKSRIRDTVCATCAENSNEHWNLTICQLCRCPDVG-- 109
QY 70 EEARACHATHNACRCRTGFFAHAGFLE--H-----ASCPGA-GVIAPGTPSQNTQCQ 122
DB 110 LEEIAFTSKRKTKCQCPQMGFC-AAWALECTHCELLSDCPGTEAEKDEKGVGNHCV 168
QY 123 PCPPGTFSSASSSECOCPHNCRTALGLNVPGSSSHDTLCTSCGFLPLSTRVPGAEC 182
DB 169 PKAGHFQNTSSSAKCPHTRCENGLVEAPGTQSDTTCRNPLE-PLPPMSGTMMLM 227
QY 183 ERAVIDFVAFQDIS-----IKRLQLLQALEAPEGWGTPPRAG 220
DB 228 LAVLLPLAFLLLATVFCSLWKSHPSLCRKLGSLLK--RRPQEGEPNPVAG 276

RESULT 4
TNRC_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LTBR OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RA MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RL and expression."
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping.";
RL Genomics 30:312-319(1995).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; U29173; AAA68964.1; -
DR EMBL; L38423; AAB00846.1; -
DR EMBL; U30798; AAA81334.1; -
DR HSSP; P25942; ICDF.
DR MGD; MGI:104875; Ltbr.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.
FT DOMAIN 224 244 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 245 415 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 213 4 X TNFR-CYS.
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 170 TNFR-CYS 3.
FT REPEAT 171 213 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 142 169 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 17.8%; Score 265.5; DB 1; Length 415;
Best Local Similarity 30.9%; Pred. No. 3.7e-14;
Matches 72; Conservative 24; Mismatches 88; Indels 49; Gaps 10;

QY 20 CAQCPGTFVQRCRDSPTTCGPPRHYTFQWNYL---ERCRCYNVLCGEREERARAC 76
DB 59 CSRCPPGEFVAVCSRSQDTCKTCHNSYNEHWNHLSLTCQLCRPCDILVG---FEVAPC 116
QY 77 HATHNACRCRTGFFAHAGFCL---EHASCPGAGVIA-PGTPSQNT-----QCQP 123
DB 117 TSDRKAECRCQPGM-----SCVYLDNECVHCEERLVLCQPGTEAEVTDIMTDVNCVP 171
QY 124 CPPTGTFSSASSSECOCPHNCRTALGLNVPGSSSHDTLCTSCGFLPLSTRVPGAEECE 183
DB 172 CKPGHFQNTSSPRARCPHTRCEIQGLVEAAPGTSYSDICK-----NPPPGAMLL 224
QY 184 RAVIDFVAF-----ODISIKRLQLLQALEAPEGWG----PTPRA 219

```


FT DOMAIN 224 283 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 162 3 X TNFR-CYS.
 FT REPEAT 42 75 TNFR-CYS 1.
 FT REPEAT 78 119 TNFR-CYS 2.
 FT REPEAT 121 162 TNFR-CYS 3.
 FT DISULFID 42 53 BY SIMILARITY.
 FT DISULFID 54 67 BY SIMILARITY.
 FT DISULFID 57 75 BY SIMILARITY.
 FT DISULFID 78 93 BY SIMILARITY.
 FT DISULFID 96 111 BY SIMILARITY.
 FT DISULFID 99 119 BY SIMILARITY.
 FT DISULFID 121 127 BY SIMILARITY.
 FT DISULFID 138 162 BY SIMILARITY.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 17 17 K > R (IN REF. 1).
 SQ SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;

Query Match 16.4%; Score 244; DB 1; Length 283;
 Best Local Similarity 37.3%; Pred. No. 1.3e-12;
 Matches 56; Conservative 14; Mismatches 68; Indels 12; Gaps 4;

QY 20 CAQCPGCTFVQRCRDSPTTCGCPPRHYTQFWNYLER---CRYCNVLCGEREEARAC 76
 Db 54 CPKCSGPGYRKEACGELTGTVCPEPGTYIAHLNGLSKLOQCQMDPAMGLR--ASRNC 111
 QY 77 HATHNRACRGTGFFA-----HAGFLEHACGPPGAGVIAPGTPSONTCQCPGCTFS 130
 Db 112 SRTEAVCGSGPHFCIVQGDHCAACRAYATSSPGORVOKGTESQDTLCQNCPPGTF 171
 QY 131 ASSSSSQCPHNRCTALGLALNVPSSSH 160
 Db 172 -PNTLEECQHOTKCSLWTKAGAGTSSSH 200

RESULT 7
 VT2_SFVKA
 ID VT2_SFVKA STANDARD; PRT; 325 AA.
 AC P25943;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS Shope fibroma virus (strain Kasza) (SFV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Leporipoxvirus.
 OX NCBI_TaxID=10272;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87321103; PubMed=2820128;
 RA Upton C., Delange A.M., McFadden G.;
 RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
 RT telomeric region of the Shope fibroma virus genome.";
 RL Virology 160:20-30(1987).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=91207415; PubMed=1850261;
 RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrar T., Upton C.,
 RA McFadden G., Goodwin R.G.;
 RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
 RT form of the TNF receptor.";
 RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
 CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M17433; ; NOT_ANNOTATED_CDS.
 DR EMBL; A23727; CAA01687.1; -.
 DR PIR; B43692; B43692.
 DR HSSP; P19438; 1TNR.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 2.
 DR ProDom; PD000771; TNFR_C6; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 1.
 KW Receptor; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
 FT DOMAIN 27 186 4 X TNFR-CYS.
 FT REPEAT 27 62 TNFR-CYS 1.
 FT REPEAT 63 104 TNFR-CYS 2.
 FT REPEAT 105 147 TNFR-CYS 3.
 FT REPEAT 148 186 TNFR-CYS 4.
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match 15.7%; Score 234.5; DB 1; Length 325;
 Best Local Similarity 32.9%; Pred. No. 8.3e-12;
 Matches 52; Conservative 19; Mismatches 76; Indels 11; Gaps 3;

QY 18 LVCAQCPGCTFVQRCRDSPTTCGCPPRHYTQFWNYLERCRYCNVLCGEREEARACH 77
 Db 38 LCCASCHPGFYASRLCGPSNTVCSPCEDGTFTASTNHAPACVSCRPCTGHLSESPQCD 97
 QY 78 ATHNRACRGTGFFA-----HAGFLEHACGPPGAGVIAPGTPSONTCQCPGTFSA 131
 Db 98 RTHDRVNCSTGNYCLLKQNGCRICAPQTKCPAGYGV-SGHTRAGDTLCKCPHPHYSD 156
 QY 132 SSSSSQCPHNRCTALGLALNVPSSSHDTLCTCTG 169
 Db 157 SLSPTERCSTGFNYISVGFNL----YPVNETSCTTTAG 190

RESULT 8
 OX40_HUMAN
 ID OX40_HUMAN STANDARD; PRT; 277 AA.
 AC P43489; Q13663;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
 DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
 GN TNFRSF4 OR TXGPI1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94170844; PubMed=7510240;
 RA Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
 RA Hummel M., Fonatsch C., Stein H.;
 RT "The human OX40 homolog: cDNA structure, expression and chromosomal
 RT assignment of the ACT35 antigen.";
 RL Eur. J. Immunol. 24:677-683(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95219871; PubMed=7704935;
 RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
 RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;

"Identification of OX40 ligand and preliminary characterization of its activities on OX40 receptor.";
Circ. Shock 44:30-34(1994).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

DR EMBL; X75962; CAAS3576.1; .
DR EMBL; S76792; AAB33944.1; ALT_INIT.
DR HSP; P25942; ICDF.
DR MIM; 600315; .
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 277 OX40L RECEPTOR.
FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 235 POTENTIAL.
FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 30 169 4 X TNFR-CYS.
FT REPEAT 30 65 TNFR-CYS 1.
FT REPEAT 66 107 TNFR-CYS 2.
FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 127 167 TNFR-CYS 4.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 14.5%; Score 215.5; DB 1; Length 277;
Best Local Similarity 27.0%; Pred. No. 2.3e-10;
Matches 72; Conservative 22; Mismatches 104; Indels 69; Gaps 11;

QY 6 TYPWRDAETGERLVCAQCPGCTFVQRCRRDSPPTCGCPRHVYTFQWNY--LERCRCYN 63
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
DB 35 TYPNSDR-----CCHCEKRGNGVMSCRSQNTVCRPGGFGFNDVSSKPCPKPCWCN 88
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 64 VLGEREEERACHATHNRCRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQCP 123
: : : : : | | | | | : : : : : | | | | | : : : : :
DB 89 LRSG--SERKQLCTATQDTCRCRAG-----TQPLDSYKPG-----VDCAP 127
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 124 CPPTGFSASSSSSQCPHNRCTALGALNVPGSSSHDTLCTS---CTGFLPLSTRVPGAE 180
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
DB 128 CPPGHF--SPGDNOACKPWTNCTLAGKHTLQPASNSDAICEDRDPATQPTQGGPPAR 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 181 ECERAVIDFAVDQISIKRLQRLQALAEPEGW-----GPTPR-----AGRAALQLKLR 230
: : : : : | | | | | : : : : : | | | | | : : : : :
DB 186 PI-----TVQTEANPRTSQGSPSTRVPGGRAVAAILGLG 222
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 231 RLTELLAQGDGALLVRLQLALVARMP 257
: : : : : | | | | | : : : : : | | | | | : : : : :
DB 223 LVGLGLGL--AILLALYLLRRDRLP 247
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

RESULT 9
OX40_RAT
ID OX40_RAT PRT; 271 AA..
AC P15725;

DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TXGP1L OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=90214614; PubMed=2157591;
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
RT lymphocytes -- a molecule related to nerve growth factor receptor.";
RL EMBO J. 9:1063-1068(1990).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

DR EMBL; X17037; CAA34897.1; .
DR PIR; S08036; S08036.
DR PIR; S12783; S12783.
DR HSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 271 OX40L RECEPTOR.
FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 235 POTENTIAL.
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 164 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 102 TNFR-CYS 2.
FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 124 164 TNFR-CYS 4.
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 14.2%; Score 211.5; DB 1; Length 271;
Best Local Similarity 31.5%; Pred. No. 4.6e-10;
Matches 53; Conservative 18; Mismatches 54; Indels 43; Gaps 8;

QY 6 TYPWRDAETGERLVCAQCPGCTFVQRCRRDSPPTCGCPRHVYTFQWNY--LERCRCYN 63
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
DB 30 TYP-----SGHK--CCRCQPGHGMVSRCDHTRDVCHPCPEGFYNEAVNYDTCQCTQCN 83
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 64 VLGEREEERACHATHNRCRCRTGFFAHAGFCLEHASCPGAGVIAPGT-PSQNT--- 119
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
DB 84 HRSG--SELKQNCPTTEDTVQCR-----PGTQPRQDSSHK 117
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 120 ---QCPCPPGTFSSASSSSSQCPHNRCTALGALNVPGSSSHDTLCL 164
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
DB 118 LGVDCVCPGPHF--SPGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

```
RESULT 10
CD40_HUMAN STANDARD; PRT; 277 AA.
AC P25942;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=89356608; PubMed=2475341;
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorath J., Aruffo A.;
RT "A B-lymphocyte activation molecule related to the nerve growth
factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
[2]
RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
the ligand binding domain of the human B cell receptor CD40.";
RL Proteins 27:59-70(1997).
[3]
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=98266353; PubMed=9605317;
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
Zhang Z., Naismith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROM; NOTE=CD guide CD40 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd40.htm".
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; X60592; CAA43045.1; -
DR PIR; S04460; S04460.
DR PDB; ICDF; 01-APR-97.
DR MIM; 109535; -
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 277 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
-----
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT CARBOHYD 153 153
FT CARBOHYD 180 180
SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;
Query Match 14.2%; Score 211; DB 1; Length 277;
Best Local Similarity 30.5%; Pred. No. 5 le-10;
Matches 46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;
OY 20 CAQCPTGTFVORPCRRDSTTCGCPRRHYTFQWNYLERC---RYCNVLCGEREEARAC 76
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
DB 38 CSLCQPGOKLVSDCTETETETCLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGT 97
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
OY 77 HATHNRACRRTGFFAHA---GFCLEHASPPGAGVIAPGPSQNTQOCPCPGTFSASS 133
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
DB 98 ET--DTICTCEGWHCTSEACSCVLHRSCTSPGFGVKQIATGVSDTICEPCPVGFFSNVS 155
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
OY 134 SSSEOCOPHRNCTALGLALNVPVSSSHDTLC 164
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
DB 156 SAFEKCHPWTSCTEKDLVVOQAGTKNTDVC 186
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
RESULT 11
VT2_MYXVL STANDARD; PRT; 326 AA.
AC P29825;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=31530;
RN [1]
RP MEDLINE=91335768; PubMed=1651597;
RA Upton C., Macen J.L., Schreiber M., McPadden G.;
RT "Myxoma virus expresses a secreted protein with homology to the tumor
necrosis factor receptor gene family that contributes to viral
virulence.";
RL Virology 184:370-382(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; M95181; AAA46632.1; -
DR EMBL; A23729; CAA01688.1; -
DR PIR; A40566; GQVZML.
DR HSSP; P19438; ITNR.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
```

```
DR PROSITE: PS00050: TNFR_NGFR_2; 2.  
KW Receptor; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 16 POTENTIAL.  
FT CHAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.  
FT DOMAIN 27 186 4 X TNFR-CYS.  
FT REPEAT 27 62 TNFR-CYS 1.  
FT REPEAT 63 104 TNFR-CYS 2.  
FT REPEAT 105 147 TNFR-CYS 3.  
FT REPEAT 148 186 TNFR-CYS 4.  
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;  
  
Query Match 14.1%; Score 210.5; DB 1; Length 326;  
Best Local Similarity 30.4%; Pred. No. 6.6e-10;  
Matches 48; Conservative 19; Mismatches 80; Indels 11; Gaps 3;  
  
QY 18 LVCAQCPGTFVQRCRDSPTTCGCPRRHYTFQWNYLERCYCNVLGGEREEARACH 77  
DB 38 LCCTSCPPGYSASRLCGPGSDTVCSCKNETFTASTNHAPACVSCRGRTGHLSESQSCD 97  
QY 78 ATHNRACRRTGFFA-----HAGFCLHASCPGAGVIAPGTPSONTOCQCPPTGESA 131  
DB 98 KTRDRVDCSAGNYCLLKQEGCRICAPTKCPAGIGV-SGHTRTGDLVLTCKPRITYSD 156  
QY 132 SSSSSQCPHRRNCTALGLALNVPGSSSHDTLCTCTG 169  
DB 157 AVSSTCTSSFNVISVEFNL-----YPVNDTSCITTAG 190  
  
RESULT 12  
CD40_MOUSE  
ID CD40_MOUSE STANDARD; PRT; 289 AA.  
AC P27512;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).  
GN TNFRSF5 OR CD40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
[1]  
RN SEQUENCE FROM N.A.  
RP Torres R.M.; Clark E.A.; PubMed-1370315;  
RX MEDLINE-92105763; PubMed-1281194;  
RA Torres R.M.; Clark E.A.;  
RT "Differential increase of an alternatively polyadenylated mRNA  
species of murine CD40 upon B lymphocyte activation."  
RL J. Immunol. 148:620-626(1992).  
RN [2]  
RP REVISIONS.  
RC STRAIN-BALB/C;  
RA Torres R.M.;  
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE FROM N.A.  
RC STRAIN-BALB/C; TISSUE=Liver;  
RX MEDLINE-93094586; PubMed-1281194;  
RA Grimaldi J.C.; Torres R.; Kozak C.A.; Chang R.; Clark E.A.;  
RA Howard M.; Cockayne D.A.;  
RT "Genomic structure and chromosomal mapping of the murine CD40 gene."  
RL J. Immunol. 149:3921-3928(1992).  
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its
```

```
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL: M83312; AAB08705.1; -  
DR EMBL: M94126; AAA37404.1; -  
DR EMBL: M94129; AAA37404.1; JOINED.  
DR EMBL: M94128; AAA37404.1; JOINED.  
DR EMBL: M94127; AAA37404.1; JOINED.  
DR PIR: A46476; A46476.  
DR HSSP: P25942; 1CDF.  
DR MGD: MGI:88336; Tnf1rsf5.  
DR InterPro: IPR001388; TNFR_c6.  
DR Pfam: PF00020; TNFR_c6; 4.  
DR ProDom: PD000771; TNFR_c6; 1.  
DR SMART: SM00208; TNFR; 4.  
DR PROSITE: PS00652; TNFR_NGFR_1; 1.  
DR PROSITE: PS00050; TNFR_NGFR_2; 4.  
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 289 CD40L RECEPTOR.  
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 194 215 POTENTIAL.  
FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 187 4 X TNFR-CYS.  
FT REPEAT 25 60 TNFR-CYS 1.  
FT REPEAT 61 103 TNFR-CYS 2.  
FT REPEAT 104 144 TNFR-CYS 3.  
FT REPEAT 145 187 TNFR-CYS 4.  
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;  
  
Query Match 13.6%; Score 203; DB 1; Length 289;  
Best Local Similarity 31.1%; Pred. No. 2.3e-09;  
Matches 47; Conservative 19; Mismatches 77; Indels 8; Gaps 3;  
  
QY 20 CAQCPGTFVQRCRDSPTTCGCPRRHYTFQWNYLERC---RYCNVLGGEREEARAC 76  
DB 38 CDLCQPGSLTSTALEKTQCHDCSGEFSQAWNRIRCHQHRHCEPNOGLRVKKEGT- 96  
QY 77 HATHNRACRRTGFFA---HAGFCLHASCPGAGVIAPGTPSONTOCQCPPTGESSASS 133  
DB 97 -ASDFVCTCKEQHCTSKDCEACAAQHTPCIPGFGVEMATEITDTVCHPCPGVFFSNQS 155  
QY 134 SSSEQCPHRRNCTALGLALNVPGSSSHDTLC 164  
DB 156 SLFEKCVPMTSCEDKNLEVLQKGTSTQTNVIC 186  
  
RESULT 13  
CD40_BOVIN  
ID CD40_BOVIN STANDARD; PRT; 269 AA.  
AC Q28203;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).  
GN TNFRSF5 OR CD40.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI_TaxID=9913;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE-97281252; PubMed-9135560;  
RX Hirano A.; Brown W.C.; Estes D.M.;  
RT "Cloning, expression and biological function of the bovine CD40  
RT homologue: role in B-lymphocyte growth and differentiation in  
RT cattle."  
RL Immunology 90:294-300(1997).
```

```

CC CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U57745; AAC48710.1; -.
CC HSSP: P25942; 1CDF.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00020; TNFR_c6; 4.
CC ProDom: PD000771; TNFR_c6; 1.
CC SMART: SM00208; TNFR; 4.
CC PROSITE: PS00652; TNFR_NGFR_1; 1.
CC PROSITE: PS00050; TNFR_NGFR_2; 1.
CC Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
CC SIGNAL 1 19 POTENTIAL.
CC CHAIN 20 >269 CD40L RECEPTOR.
CC DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 194 215 POTENTIAL.
CC DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 25 187 4 X TNFR-CYS.
CC REPEAT 25 60 TNFR-CYS 1.
CC REPEAT 61 103 TNFR-CYS 2.
CC REPEAT 104 144 TNFR-CYS 3.
CC REPEAT 145 187 TNFR-CYS 4.
CC CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC NON_TER 269 269
CC SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;

Query Match 13.5%; Score 202; DB 1; Length 269;
Best Local Similarity 28.5%; Pred. No. 2.6e-09;
Matches 67; Conservative 20; Mismatches 122; Indels 26; Gaps 7;

QY 18 LVCAQCPGTFVQPCRRDSPPTTCGPPRHVYTFQFN---YLERCRVNCVLGEREEA- 73
Db 36 LCDCLPGGKLVNDCTEVSKCQSGKGEFLSTWNREKYCHEHRYCNPNLGLRIQSEG 95
QY 74 -----RACHATHNRACRCRTGFFAHAGFCLHASCPCPGAGVAPGTPSQTQCPQPGT 128
Db 96 TLNTDTICVCEGOHCTSHT-----CESCTPHSLCLPGFGVKQIATGLLDTVCPCPLGF 150
QY 129 FSASSSSQCPHNRCTALGLALNVPGSSSHDTLCTSCGFPPLSTRVPGAECERAVID 188
Db 151 FSNVSSAFERCHRTSCERKGLVEQHVGNKTDVVC---GFQSRMRTLVIPIVTMGVLF 206
QY 189 FVAFQDISIKRLQRLQALPEAGWGTPPRAGAAQLQLRRRL---TELLGAQD 240
Db 207 AVLLVSCIRNITKQK-LRPCTLW-----LGRIPWRRLIRIRFPAPTRLUGARD 256

RESULT 14
OX40_MOUSE STANDARD; PRT; 272 AA.
AC P47741;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
GN TNFRSF4 OR TXGP1 OR OX40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=BALB/C;
RX MEDLINE=94044750; PubMed=8228223;
RA Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
RA Claassen E., Noelle R.J., Fell H.;
RT "Cloning of mouse OX40; a T cell activation marker that may mediate
RL T-B cell interactions."
RN J. Immunol. 151:5261-5271(1993).
RP SEQUENCE FROM N.A.
RX MEDLINE=95255413; PubMed=7737295;
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Barclay A.N.;
RT "Gene structure and chromosomal localization of the mouse homologue
RL of rat OX40 protein."
RL Eur. J. Immunol. 25:926-930(1995).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z11674; CAA79772.1; -.
CC EMBL: X85214; CAA59476.1; -.
CC HSSP: P25942; 1CDF.
CC MGD: MGI:104512; Tnfrsf4.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00020; TNFR_c6; 3.
CC ProDom: PD000771; TNFR_c6; 1.
CC SMART: SM00208; TNFR; 3.
CC PROSITE: PS00652; TNFR_NGFR_1; 3.
CC PROSITE: PS00050; TNFR_NGFR_2; 2.
CC Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT CHAIN 1 19 POTENTIAL.
FT DOMAIN 20 272 OX40L RECEPTOR.
FT TRANSMEM 212 236 POTENTIAL.
FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 13.0%; Score 194.5; DB 1; Length 272;
Best Local Similarity 30.4%; Pred. No. 1e-08;
Matches 51; Conservative 16; Mismatches 58; Indels 43; Gaps 8;

QY 6 TYPWDAETGERLVCAQCPGTFVQPCRRDSPPTTCGPPRHVYTFQFN---LERCRVNC 63
Db 31 TYP-----SGHK-CCRECQPGHGMVSRCDTRDTLCHPCETGFYNEAVNDTKQCTQC 84
QY 64 VLCGEREEARACHATHNRACRCRTGFFAHAGFCLHASCPCPGAGVAPGT-PSQNT--- 119
Db 85 HRSG--SELKQNCPTPTQDTCRCR-----PQTQPRQDSGYK 118
QY 120 ---QCPCPPGTFSSASSSSQCPHNRCTALGLALNVPGSSSHDTLCL 164
Db 119 LGVDCVPCPPGPHF--SPGNNAQCKPWTNCTLSGKQTRHRPASDILDVAVC 164

RESULT 15
41BB_MOUSE

```

ID AC 41BB_MOUSE STANDARD; PRT; 256 AA.
DT P20334;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).
GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=89184547; PubMed=2784565;
RX Kwon B.S., Weissman S.M.;
RA "CDNA sequences of two inducible T-cell genes.";
RT Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=BALB/C;
RX MEDLINE=94179805; PubMed=8133039;
RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
RT "Genomic organization and chromosomal localization of the T-cell
antigen 4-1BB.";
RL J. Immunol. 152:2256-2262(1994).
RN [3]
RN CHARACTERIZATION, AND SEQUENCE OF 25-29.
RX MEDLINE=93139510; PubMed=7678621;
RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kim K.K., Pickard R.T.,
RA Kwon B.S.;
RT "Inducible T cell antigen 4-1BB. Analysis of expression and
function.";
RL J. Immunol. 150:771-781(1993).
CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
ACTIVE DURING T CELL ACTIVATION.
CC -1- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
CC ASSOCIATES WITH P56-LCK.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
CC -1- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; J04492; AAA40167.1; -;
DR EMBL; U02567; AAA93113.1; -;
DR PIR; B32393; B32393.
DR HSSP; P25942; 1CDF.
DR MGD; MGI:1101059; Tnfrsf9.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; FALSE_NEG.
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 25 256 4-1BB LIGAND RECEPTOR.
FT DOMAIN 25 187 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 208 POTENTIAL.
FT DOMAIN 209 256 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 17 159 4 X TNFR-CYS.
FT REPEAT 17 45 TNFR-CYS 1.
FT REPEAT 46 85 TNFR-CYS 2.
FT REPEAT 86 117 TNFR-CYS 3.
FT REPEAT 118 159 TNFR-CYS 4.
FT CARBOHYD 128 128 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;
Query Match 12.4%; Score 185; DB 1; Length 256;
Best Local Similarity 28.3%; Pred. No. 5.4e-08;
Matches 65; Conservative 24; Mismatches 85; Indels 56; Gaps 14;
QY 20 CAQCPPGTFFVORPCRRDSPTTTCGCPPPRHYTQFWNYLERCRYCNVLCGEREEARACHAT 79
DB 28 CDNCOPGT-----CRKYNP-VCKSCPPSTFSSIGQ-PNCNICRV-CAGYFRFKFCST 80
QY 80 HNRACRCRTGFFAHAGFCLE-HASCPGAGVIAPGTPTSONTOCQPCPGTTSASSSSSEQ 138
DB 81 HNAECIEGPHCLGPOCTRCCKDCRPOELTKQ-----CKTCSLGTFN-DONGTGV 132
QY 139 CQPHRNTALGLALNVPGSSSHDTLCTSTCTGFPPLSTRVPGAEECEERAVIDFVAFODISIK 198
DB 133 CRPWTNCSLDGRSVLKTGTTEKDVVC-----GPP-----VVSFSPSTTISV- 173
QY 199 RLQRLQALEAPEGWGTPPRAGRAALQLKRLRLTELLGAODGALLVRL 248
DB 174 -----TPEG-GP-----GGHSLQV-----LTLFL-ALTSALLALI 202

Search completed: May 10, 2002, 10:59:24
Job time: 333 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:54:20 ; Search time 24.1 Seconds
(without alignments)
856.569 Million cell updates/sec

Title: US-09-280-567-6
Perfect score: 1491
Sequence: 1 VAETTPWRDAETGERLVC.....RVAMPGLERSVRERFLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	340.5	22.8	461	1	A35356 tumor necrosis fac
2	333.5	22.4	459	2	I48854 gene murine tumour
3	332.5	22.3	474	2	B38634 tumor necrosis fac
4	299.5	20.1	435	2	I54182 tumor necrosis fac
5	260	17.4	348	2	T28623 hypothetical prote
6	260	17.4	349	2	D72175 G2R protein - vari
7	260	17.4	349	2	D36858 gene G4R protein -
8	234.5	15.7	325	2	B43692 T2 protein - rabbi
9	215.5	14.5	277	2	I37552 OX40 homolog - hum
10	211.5	14.2	271	2	S12783 OX40 antigen precu
11	211	14.2	277	2	A60771 B-cell activation
12	210.5	14.1	326	1	QOVZML T2 protein - myxom
13	203	13.6	305	2	A46706 B cell-associated
14	194.5	13.0	272	2	I48700 gene ox40 protein
15	185	12.4	256	2	B32393 T-cell antigen 4-1
16	182	12.2	595	2	A42086 CD30 antigen precu
17	174	11.7	255	2	I38426 lymphocyte activat
18	171.5	11.5	416	1	JN0006 nerve growth facto
19	168	11.3	425	1	A26431 nerve growth facto
20	158	10.6	427	1	QGHUN nerve growth facto
21	155.5	10.4	327	2	A46484 apoptosis-mediati
22	148.5	10.0	1574	2	T13954 MSGF6 protein - ra
23	148	9.9	250	1	A49053 CD27 antigen precu
24	147.5	9.9	5376	1	T42215 zonadhesin - mouse
25	146.5	9.8	260	1	A46517 CD27 antigen precu
26	145	9.7	335	2	A40036 apoptosis-mediati
27	143	9.6	1620	2	T27283 hypothetical prote
28	140	9.4	314	2	I37383 FAS soluble protei
29	137.5	9.2	324	2	JC2395 Fas antigen precu

30 135.5 9.1 1299 2 T43251 furin (EC 3.4.21.7
31 135 9.1 2321 2 S78549 notch3 protein - h
32 130.5 8.8 454 1 GOMST1 tumor necrosis fac
33 128.5 8.6 3635 2 T10053 laminin alpha 5 ch
34 127 8.5 1192 2 S69000 laminin gamma 2 ch
35 125.5 8.4 1548 2 S34583 serine proteinase
36 124.5 8.4 1713 2 A55347 adhesive ligand ep
37 123.5 8.3 455 1 GQHUT1 tumor necrosis fac
38 123.5 8.3 493 2 JC5486 membrane glycoprot
39 122.5 8.2 2824 2 T22759 hypothetical prote
40 121 8.1 3106 1 S53868 laminin alpha-2 ch
41 120 8.0 1609 1 MMHUB2 laminin gamma-1 ch
42 119.5 8.0 3084 1 MMMSA laminin alpha-1 ch
43 118.5 7.9 461 1 GQRTT1 tumor necrosis fac
44 118.5 7.9 1680 2 A43434 furin (EC 3.4.21.7
45 118 7.9 899 2 G02428 subtilisin-like pr

ALIGNMENTS

RESULT 1

A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a
A:Reference number: A35356; MUID:90260639
A:Accession: A35356
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SM>
A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R:Kolomo, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
A:Reference number: A36475; MUID:91045991
A:Accession: A36475
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195; 'R', 197-461 <KOH>
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular
A:Reference number: A48416; MUID:91370690
A:Accession: A48416
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 23-461 <DEM>
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:63371)
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons
A:Reference number: A36007; MUID:90349572
A:Accession: A36007
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140; 'P', 142-195; 'R', 197-362; 'T', 364-461 <HEL>
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63562.1; PID:g339752
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor
A:Reference number: A23666; MUID:91056048
A:Accession: A23666
A:Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>

R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C;Genetics:
A;Gene: GDB:TNFR2
A;Cross-references: GDB:I25914; OMIM:191191
A;Map position: lp36.2-lp36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.8%; Score 340.5; DB 1; Length 461;
Best Local Similarity 29.7%; Pred. No. 1.3e-18;
Matches 89; Conservative 43; Mismatches 115; Indels 53; Gaps 11;

Qy 1 VAETPTYPWRDAETGE-----RLVCAQCPGTFVQRCRDRSDPTTCGCPGPRH 48
Db 27 VAFTYAP-----EPGSTCLREYDQTAQMCCKSCSGQHAQVCTKTSVTCDSCEDET 82
Qy 49 YTOFWNYLERCRYCNVLGGEREEPARACHATHNACRCRTGFFAHAG-----FCLHAS 102
Db 83 YTQLNWNVPECLSCGSCSSDQVETOACTREQNRICTRCPGWCYALSKQECRCICAPLRK 142
Qy 103 CPPGAGVIAGTPSQNTQCPCPGTFSASSSEQCPHNCRTALGLALNVPSSSHDT 162
Db 143 CRPGFGVAREGTETSDVVCPCAPGTFSTNTSSTDICRPHQICNVVA-----IPGNASMDA 198
Qy 163 LCTSCGFLPLSTRVPGAEECEERAVDFVAFQDISIKRLQLRLQALEAPE-----GWGPTP 217
Db 199 VCTRST--PFRMAPGAVHLPQV-----STRSQITQTPPESTAPSTFLLPMGSP 249
Qy 218 RA-----GRAALQLKRLRLTELLGAODGALLVRLQLAL---RVARMPLGLERSVREFLP 269
Db 250 PAEGSTGDFALPVGLIVGVTA-----GLLIIGVNCVINTQVKKKPLCLQREAKVPHLP 304

RESULT 2
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848
A;Accession: I48854
A;Status: preliminary; translated from GB/EMBL/DBJ

Query Match 22.3%; Score 332.5; DB 2; Length 474;

A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 22.4%; Score 333.5; DB 2; Length 459;
Best Local Similarity 29.7%; Pred. No. 4.5e-18;
Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;

Qy 17 RLVCAQCPGTFVQRCRDRSDPTTCGCPGPRHYTFQWNYLERCRYCNVLGEREEPARAC 76
Db 37 QMCCAKCPGQYVRFHFNKTSDTVCADCEASWYQVNMQFRTCLSCSSCSCTDQVETRAC 96
Qy 77 HATHNRACRCRTGTF-----AHAGF---CLEHASCPPGAGVIAGTPSQNTQCPCPGTFF 129
Db 97 TKQNRVCAACEAGRYCALKTHSGSCRCQCMRLSKGPGFVASSRAPNGNVLCACAPGTF 156
Qy 130 SASSSSSEQCPHNCRTALGLALNVPSSSHDTLCT-----SCTGFPLSTRVPGAEECEA 185
Db 157 SDTTSSTDVCRPHRICSLA----IPGNASTDAVCAPESPTLSAIPRPLYVSQEPETRSQ 212
Qy 186 VIDFVAFQDISIKRLQLRLQALEAPEGWPPTP-----RAGRAALQLKRLRLTELLGAOD 240
Db 213 PLD-----QEPGFSQTPSILTSL-----GSTPIIEQSTKGGISLPIGLIVGVTSLSL 257
Qy 241 GALLVRLQLAL---RVARMPLGLERSVREFLP 269
Db 258 GLLMLGLVNCFILVORKKPKSCLQORDAKRVHPV 290

RESULT 3
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A;Reference number: A38634; MUID:91187885
A;Accession: B38634
A;Molecule type: mRNA
A;Residues: 1-474 <LEW>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A;Reference number: A40254; MUID:91246168
A;Accession: A40254
A;Molecule type: mRNA
A;Residues: 1-474 <GOO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kisssonerghis, M.; Fallowes, R.; Feldmann, M.; Chernajovsky, Y.
Submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor
A;Reference number: S54816
A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>

R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; *et al.*
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox vir
A:Reference number: Z20488; MUID:94088747
A:Accession: T28623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A:Experimental source: strain Bangladesh 1975
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 348;
Best Local Similarity 32.2%; Pred. No. 1.3e-12;
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

Qy 5 PYPWRDAE-TGERLVCAOCPPGTFVQRCRRDSPITCGPCPPRHYTQFWNYLERCRYCN 63
Db 27 PNGKCKDTEYKRNHLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 86
Qy 64 VLCGEREEARACHATHNACRRTGFF-----AHAGFCLEHASCPCPGAGVIAPGTPSQ 117
Db 87 GRCSNQVETRCNTTHNRCICESPGYICLLKGSSGCKACVSQTKCGIGYV-SGHTSVG 145
Qy 118 NTQOCPCPPGTFSSSSSEOCOPHRNCTALGIALNVPGSSSHDTLCTSCGFFPLSTRVP 177
Db 146 DVICSPGFGTGYTSVSSDADKCEVPNNTFNYIDVEITLIPVNDTCTRTTTTGLSESIL 205
Qy 178 GAE 180
Db 206 TSE 208

RESULT 6
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C:Accession: D72175
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; *et al.*
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola mi
A:Reference number: A72150
A:Accession: D72175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: G2R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 349;
Best Local Similarity 32.2%; Pred. No. 1.3e-12;
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

Qy 5 PYPWRDAE-TGERLVCAOCPPGTFVQRCRRDSPITCGPCPPRHYTQFWNYLERCRYCN 63
Db 28 PNGKCKDTEYKRNHLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 87
Qy 64 VLCGEREEARACHATHNACRRTGFF-----AHAGFCLEHASCPCPGAGVIAPGTPSQ 117
Db 88 GRCSNQVETRCNTTHNRCICESPGYICLLKGSSGCKACVSQTKCGIGYV-SGHTSVG 146
Qy 118 NTQOCPCPPGTFSSSSSEOCOPHRNCTALGIALNVPGSSSHDTLCTSCGFFPLSTRVP 177
Db 147 DVICSPGFGTGYTSVSSDADKCEVPNNTFNYIDVEITLIPVNDTCTRTTTTGLSESIL 206
Qy 178 GAE 180
Db 206 TSE 208

Db 207 TSE 209

RESULT 7

D36858

gene G4R protein - variola virus

N;Alternate names: B28R protein (COP)

C;Species: variola virus

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001

R;Blinov, V.M.

Submitted to GenBank, November 1992

A;Reference number: A36859

A;Accession: D36858

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-349 <BLI>

A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087

A;Experimental source: strain India-1967, ssp. major, isolate Ind3

R;Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, V.V.

submitted to the EMBL Data Library, April 1992

A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P

A;Reference number: S46868

A;Accession: S46888

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-349 <ROL>

A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449

A;Experimental source: strain India-1967, isolate Ind3

R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.

FEBS Lett. 319, 80-83, 1993

A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A;Reference number: S32385; MUID:93202281

A;Accession: S32385

A;Molecule type: DNA

A;Residues: 1-168 <SHC>

A;Cross-references: EMBL:X69198

A;Experimental source: strain India-1967, ssp. major

C;Genetics:

A;Gene: G4R

C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F;32-66/Domain: NGF receptor repeat homology <NGF>

F;68-109/Domain: NGF receptor repeat homology <NG3>

F;110-151/Domain: NGF receptor repeat homology <NG3>

Query Match

Best Local Similarity 17.4%; Score 260; DB 2; Length 349;

Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCCRRDSPPTTCGPPRRHYTFQWNYLERCRYCN 63

Db 28 PNGKCKDTEYKRNLCLSCPPGTIYASRLCDSKTNTQCTPCGSGTFTSRNHLPACLSCN 87

QY 64 VLGEREEERACHATHNRACRGTGFF-----ANIAGFCLEHASCPPGAGVIAPGTPSQ 117

Db 88 GRNSNQVETRSCNTTHNRICEGSPGYICLLKSGSGKACVQSKTCGIGYGV-SGHTSVG 146

QY 118 NTCQCPCCPTTFSSASSSEOCOPHRNCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVP 177

Db 147 DVTCSPCGCTGTYSHTVSSADKCEPVNPNFNYIDVEITLYPVNDTCTCTRTTTGLSESL 206

QY 178 GAE 180

Db 207 TSE 209

RESULT 8

B43692

T2 protein - rabbit fibroma virus

C;Species: rabbit fibroma virus, Shope fibroma virus

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: B43692

R;Upton, C.; DeLange, A.M.; McFadden, G.

Virology 160, 20-30, 1987

A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer

A;Reference number: A43692; MUID:87321103

A;Accession: B43692

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 <UPT>

A;Cross-references: GB:M17433

C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F;64-105/Domain: NGF receptor repeat homology <NG2>

F;106-147/Domain: NGF receptor repeat homology <NG3>

Query Match

Best Local Similarity 15.7%; Score 234.5; DB 2; Length 325;

Matches 52; Conservative 19; Mismatches 76; Indels 11; Gaps 3;

QY 18 LVCAQCPPGTFVQRPCCRRDSPPTTCGPPRRHYTFQWNYLERCRYCNVLCGEREEARACH 77

Db 38 LCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCRCGCTGHLSESQPCD 97

QY 78 ATHNRACRGTGFFA-----HAGFCLEHASCPPGAGVIAPGTPSQNTQCPGPTFSA 131

Db 98 RTHDRVNCSTGNYCLLKGGNGCRICAPQTKCPAGYGV-SGHTRAGDTLCKECPHTYSD 156

QY 132 SSSSEOCOPHRNCTALGLALNVPGSSSHDTLCTCTG 169

Db 157 SLSPTERCGTFNYSVIGFNL----YVPNETSCITTAG 190

RESULT 9

I37552

OX40 homolog - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000

C;Accession: I37552

R;Latza, U.; Durrkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo

Eur. J. Immunol. 24, 677-683, 1994

A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment

A;Reference number: I37552; MUID:94170844

A;Accession: I37552

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-277 <RES>

A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958

C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match

Best Local Similarity 14.5%; Score 215.5; DB 2; Length 277;

Matches 72; Conservative 22; Mismatches 104; Indels 69; Gaps 11;

QY 6 TYPRDAETGERLVCAQCPPGTFVQRPCCRRDSPPTTCGPPRRHYTFQWNY--LERCRYCN 63

Db 35 TYPNDR-----CCECRFGNGMVSRCSQNTVCRPGCGFYNDVYVSKPKCKPCTWCN 88

QY 64 VLGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCP 123

Db 89 LRSG--SERKQLCTATQDTCRCRAG-----TOPLDSYKPG-----VDCAP 127

QY 124 CPGTFSASSSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGA 180

Db 128 CPPGHF--SPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPATQPTQGGPAR 185

QY 181 ECERAVIDFVAFQDISIKRLQRLQLEAPEGW-----GTPPR-----AGRAALQLKLR 230

Db 186 PI-----TQPTAMPRTSQSPSTRPVEVPGGRAVAAILGLG 222

QY 231 RLTELLGAQDGALLVRLQLQALRVARP 257

Db 223 LVLLGLGLP--AILLALYLLRRQRLP 247

```
RESULT 10
SI2783
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: SI2783; S08036
R:Malet, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
A:Reference number: SI2783; MUID:90214614
A:Accession: SI2783
A:Molecule type: mRNA
A:Residues: 1-271 <MAT>
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C:Superfamily: CD27 antigen; NGF receptor repeat homolog
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TMM>

Query Match 14.2%; Score 211.5; DB 2; Length 271;
Best Local Similarity 31.5%; Pred. No. 4.7e-09;
Matches 53; Conservative 18; Mismatches 54; Indels 43; Gaps 8;
QY 6 TYPWRDAETGERLVCAQCPGTFVORPCRRDSPPTTCGCPPRHYTQFWNY--LERCRYCN 63
DB 30 TYP-----SGHK-CCEQCPGHWVSRCDHTRDTVCHPCPEGFYNEAVNYDKCKQCTQCN 83
QY 64 VLGGEREERACHATHNRACRCRTGFFAHAGFLEHASCPPGAGVIAGT-PSQNT--- 119
DB 84 HRSQ--SELKQNTPTEDTVCCQ-----PGTOPRODSSHK 117
QY 120 ---QCQCPGPTFSASSSSSECOCPHRNCTALGLALNVPGSSSHDTLC 164
DB 118 LGVDCVCPGPHF--SPGSNQACKPWNTCTLSGKQIRHPASNSLDIVC 163

RESULT 11
A60771
B:cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C>Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor.
A:Reference number: S04460; MUID:89356608
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R:Braesch-Andersen, S.; Paulite, S.; Kohn, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-11k
A:Reference number: A60771; MUID:89093941
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homolog
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TMM>
```

```
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.2%; Score 211; DB 2; Length 277;
Best Local Similarity 30.5%; Pred. No. 5.3e-09;
Matches 46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;
QY 20 CAQCPGTFVORPCRRDSPPTTCGCPPRHYTQFWNYLERC---RYCNVLGGEREEARAC 76
DB 38 CSLCQPGQKLVSDCTETETELCPGCESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTS 97
QY 77 HATHNRACRCRTGFFAFAH---GFCLEHASCPPGAGVIAGTTPSQNTQCCQCPGPTFSASS 133
DB 98 ET-DTICTCEGWHCTSEACSVLHRSCPGFKQIATGVSDTICEPCPVGFFSNVS 155
QY 134 SSSECOCPHRNCTALGLALNVPGSSSHDTLC 164
DB 156 SAFERCHPWTSCETKDLVVQOAGTNKTDVVC 186

RESULT 12
GOVZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: A40566
R:Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virol. 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A:Reference number: A40566; MUID:91335768
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <UPT>
A:Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homolog
C:Keywords: glycoprotein
F:64-105/Domain: NGF receptor repeat homolog <NG2>
F:106-147/Domain: NGF receptor repeat homolog <NG3>
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.1%; Score 210.5; DB 1; Length 326;
Best Local Similarity 30.4%; Pred. No. 6.7e-09;
Matches 48; Conservative 19; Mismatches 80; Indels 11; Gaps 3;
QY 18 LVCAQCPGPTFVORPCRRDSPPTTCGCPPRHYTQFWNYLERCRYCNVLGGEREEARACH 77
DB 38 LCCTSCPPGSYASRLCGPGSDTVCSCKNETFTASTNHAPACVSCRCRCTGHLSESQSD 97
QY 78 ATHNRACRCRTGFFA-----HAGFLEHASCPPGAGVIAGTTPSQNTQCCQCPGPTFSA 131
DB 98 KTRDRVDCDSAGNYCLLKGOEGCRICAPKTKPAGYGV-SGHTRTGDLCTKCPRTYSD 156
QY 132 SSSSSQCPQHRNCTALGLALNVPGSSSHDTLCSTCTG 169
DB 157 AVSSTCTSSSFYISVEFNL-----YPVNDTCTTTAG 190

RESULT 13
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A46476; A46515
R:Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of mur
A:Reference number: A46476; MUID:92105763
A:Accession: A46476
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
```

Query Match 13.0%; Score 194.5; DB 2; Length 272;
Best Local Similarity 30.4%; Pred. No. 9.2e-08;
Matches 51; Conservative 16; Mismatches 58; Indels 43; Gaps 8;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:53:03 ; Search time 22.98 Seconds
(without alignments)
265.378 Million cell updates/sec

Title: US-09-280-567-6
Perfect score: 1491
Sequence: 1 VASTPPWRDAETGERLVC.....RVAMPGLSRRERFLPVH 271

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1491	100.0	300	2	US-08-794-796-2
2	1476.5	99.0	299	4	US-09-286-529-17
3	1034	69.3	211	4	US-09-286-529-20
4	841	56.4	153	4	US-09-286-529-2
5	440.5	29.5	401	3	US-08-974-022-6
6	440.5	29.5	401	4	US-09-042-785A-12
7	440.5	29.5	401	4	US-08-795-445A-6
8	440.5	29.5	401	4	US-08-795-447A-6
9	440.5	29.5	401	4	US-08-974-186-6
10	440.5	29.5	401	4	US-08-795-446B-6
11	440.5	29.5	401	4	US-09-153-927-1
12	425.5	28.5	401	3	US-08-974-022-2
13	425.5	28.5	401	4	US-08-795-445A-2
14	425.5	28.5	401	4	US-08-795-447A-2
15	425.5	28.5	401	4	US-08-974-186-2
16	425.5	28.5	401	4	US-08-795-446B-2
17	424.5	28.5	401	3	US-08-974-022-4
18	424.5	28.5	401	4	US-09-042-785A-13
19	424.5	28.5	401	4	US-08-795-445A-4
20	424.5	28.5	401	4	US-08-795-447A-4
21	424.5	28.5	401	4	US-08-974-186-4
22	424.5	28.5	401	4	US-08-795-446B-4
23	342.5	23.0	461	4	US-09-042-785A-7
24	342.5	23.0	461	4	US-09-006-353A-4
25	340.5	22.8	461	1	US-08-385-229-2
26	340.5	22.8	461	2	US-08-650-000-2
27	340.5	22.8	461	4	US-08-477-347-3

28	340.5	22.8	461	4	US-08-476-862-2	Sequence 2, Appli
29	340.5	22.8	461	6	5395760-2	Patent No. 5395760
30	335	22.5	227	3	US-08-974-022-48	Sequence 48, Appl
31	335	22.5	227	4	US-08-795-445A-48	Sequence 48, Appl
32	335	22.5	227	4	US-08-795-447A-48	Sequence 48, Appl
33	335	22.5	227	4	US-08-974-186-48	Sequence 48, Appl
34	335	22.5	227	4	US-08-795-446B-48	Sequence 48, Appl
35	335	22.5	235	4	US-09-326-394-4	Sequence 4, Appl
36	333	22.3	486	1	US-08-243-010-1	Sequence 1, Appl
37	333	22.3	518	1	US-08-385-229-4	Sequence 4, Appl
38	332.5	22.3	474	2	US-08-650-000-4	Sequence 8, Appl
39	332.5	22.3	474	4	US-09-042-785A-8	Sequence 8, Appl
40	332.5	22.3	474	6	5395760-4	Patent No. 5395760
41	318	21.3	163	2	US-08-219-237B-5	Sequence 5, Appl
42	318	21.3	163	4	US-08-477-347-13	Sequence 13, Appl
43	318	21.3	163	4	US-08-476-862-4	Sequence 4, Appl
44	318	21.3	163	4	US-08-468-560C-5	Sequence 5, Appl
45	316	21.2	164	2	US-08-232-087A-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-794-796-2
; Sequence 2, Application US/08794796
; Patent No. 5885800
; GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,796
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH50000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-794-796-2

Query Match 100.0% Score 1491; DB 2; Length 300;

```

Best Local Similarity 100.0%; Pred. No. 2.3e-124;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAOCPPGTFVORPCRRDSTTCGPPRRHYTQFWNYLERCR 60
DB 30 VAETPTYPWRDAETGERLVCAOCPPGTFVORPCRRDSTTCGPPRRHYTQFWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 120
DB 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 149
QY 121 CQCPPTGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTRVPGAE 180
DB 150 CQCPPTGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTRVPGAE 209
QY 181 ECERAVIDFVAFODISIKRLQLLQALEAPEGWGTPPRAGRAALQKLRRRLTELLGAQD 240
DB 210 ECERAVIDFVAFODISIKRLQLLQALEAPEGWGTPPRAGRAALQKLRRRLTELLGAQD 269
QY 241 GALLVRLLOALRVARMPLGLSVRERFLPVH 271
DB 270 GALLVRLLOALRVARMPLGLSVRERFLPVH 300

RESULT 2
US-09-286-529-17
; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-17

Query Match 99.0%; Score 1476.5; DB 4; Length 299;
Best Local Similarity 99.6%; Pred. No. 4.4e-123;
Matches 270; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VAETPTYPWRDAETGERLVCAOCPPGTFVORPCRRDSTTCGPPRRHYTQFWNYLERCR 60
DB 30 VAETPTYPWRDAETGERLVCAOCPPGTFVORPCRRDSTTCGPPRRHYTQFWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 120
DB 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 149
QY 121 CQCPPTGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTRVPGAE 180
DB 150 CQCPPTGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTRVPGAE 208
QY 181 ECERAVIDFVAFODISIKRLQLLQALEAPEGWGTPPRAGRAALQKLRRRLTELLGAQD 240
DB 209 ECERAVIDFVAFODISIKRLQLLQALEAPEGWGTPPRAGRAALQKLRRRLTELLGAQD 268
QY 241 GALLVRLLOALRVARMPLGLSVRERFLPVH 271
DB 269 GALLVRLLOALRVARMPLGLSVRERFLPVH 299

RESULT 3
US-09-286-529-20
; Sequence 20, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:

```

```

; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-20

Query Match 69.3%; Score 1034; DB 4; Length 211;
Best Local Similarity 98.9%; Pred. No. 3.7e-84;
Matches 179; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAOCPPGTFVORPCRRDSTTCGPPRRHYTQFWNYLERCR 60
DB 30 VAETPTYPWRDAETGERLVCAOCPPGTFVORPCRRDSTTCGPPRRHYTQFWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 120
DB 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 149
QY 121 CQCPPTGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTRVPGAE 180
DB 150 CQCPPTGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTRVPGAE 209
QY 181 E 181
DB 210 E 210

RESULT 4
US-09-286-529-2
; Sequence 2, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
US-09-286-529-2

Query Match 56.4%; Score 841; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.9e-67;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 LERCRCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTP 115
DB 1 LERCRCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTP 60
QY 116 SONTQCPCPPGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTR 175
DB 61 SONTQCPCPPGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTR 120
QY 176 VPGAEECERAVIDFVAFODISIKRLQLLQALE 208
DB 121 VPGAEECERAVIDFVAFODISIKRLQLLQALE 153

RESULT 5
US-08-974-022-6

```

```

: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/042,785A
: FILING DATE: 17-MAR-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/938,896
: FILING DATE: 26-SEP-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Mandragouras, Amy E
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: MEI-001CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 401 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: US-09-042-785A-12
:
: Query Match 29.5%; Score 440.5; DB 4; Length 401;
: Best Local Similarity 41.2%; Pred. No. 2.3e-31;
: Matches 77; Conservative 31; Mismatches 74; Indels 5
:
: QY 5 PTVPMDAETGERLYVCAQCPGPTFVQRCRDRSPPTCGCPPRHVTQFWNYLERCR
: Db 26 PKYLHYDEETSHOLLKDKCPGPGTYLKQHCIAKWKTVCACPDPHYTTDSWHTSDECI
: QY 65 LCGEREERARACHATHNRACRGTGFAGHAGCLHEASCPGAGVIADCTPSPQNTQ
: Db 86 VKLEQYVQECNRTNHRVRCCKEGRYLEIFCLKHRSCPPGFGVVGQAGTPPRTV
: QY 125 PPGTSASSSSBQCPHRNCKTALGLANVPGSSSHDTLCTCTGFPPLSTRVPGAEB
: Db 146 PDGFFNEYSKAPCRKHNTCSVFGLLLTQKNATHDNI---CSGNSESTQCGKID
: QY 183 ERAVIDF 189
: Db 203 EEAFFR 209
:
: RESULT 7
: US-08-795-445A-6
: Sequence 6, Application US/08795445A
: Patent No. 6284485
: GENERAL INFORMATION:
: APPLICANT: Boyle, William J.
: APPLICANT: Lacey, David L.
: APPLICANT: Calzone, Frank J.
: APPLICANT: Chang, Ming-Shi
: TITLE OF INVENTION: OSTEOPROTEGERIN
: NUMBER OF SEQUENCES: 53
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen Inc.
: STREET: 1840 Behavilland Drive
: CITY: Thousand Oaks
: STATE: California
: COUNTRY: USA
: ZIP: 91320-1789
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

```

REFERENCE/DOCKET NUMBER: A-378

Query Match 29.5%; Score 440.5; DB 4; Length 401;

Query Match 28.5%; Score 425.5; DB 4; Length 401;
Best Local Similarity 39.5%; Pred. No. 4.9e-30;
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;
QY 5 PYPWRDAETGERLVCAQCQPPGTFVORPCRRDPSPTTCGCPPRHYTQFWNYLERCRCYCNV 64
DB 26 PKYLHYDPETGRQLCDKCAPCTYLKQHTVRRKTLVCPDPSYSDSWHTSDECVYCSP 85
QY 65 LCGEREEARACHATHNRACRRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTOCQPC 124
DB 86 VKELQTVKQECNRTHNRVCEEGRYLEFCLKHRSCPPGLGVLOAGTPERTVCKRC 145
QY 125 PPGTFSASSSSQCPHNRCTALGLALNVPSSSHDTLTCTSGTGFPLSTRVPGAE--C 182
DB 146 PDGFFSGETSSKAPCRKHTNCSSLSGLLLIQGNATHDNV---CSGNREATQCGIDVTL 202
QY 183 ERAVIDFVAFQDISIKRLQRLQAL 207
DB 203 EEAFFRFAVPTKIIPNWLVLVDSL 227

RESULT 15
US-08-974-186-2
; Sequence 2, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-186-2

Query Match 28.5%; Score 425.5; DB 4; Length 401;
Best Local Similarity 39.5%; Pred. No. 4.9e-30;
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;
QY 5 PYPWRDAETGERLVCAQCQPPGTFVORPCRRDPSPTTCGCPPRHYTQFWNYLERCRCYCNV 64
DB 26 PKYLHYDPETGRQLCDKCAPCTYLKQHTVRRKTLVCPDPSYSDSWHTSDECVYCSP 85

QY 65 LCGEREEARACHATHNRACRRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTOCQPC 124
DB 86 VKELQTVKQECNRTHNRVCEEGRYLEFCLKHRSCPPGLGVLOAGTPERTVCKRC 145
QY 125 PPGTFSASSSSQCPHNRCTALGLALNVPSSSHDTLTCTSGTGFPLSTRVPGAE--C 182
DB 146 PDGFFSGETSSKAPCRKHTNCSSLSGLLLIQGNATHDNV---CSGNREATQCGIDVTL 202
QY 183 ERAVIDFVAFQDISIKRLQRLQAL 207
DB 203 EEAFFRFAVPTKIIPNWLVLVDSL 227

Search completed: May 10, 2002, 10:53:03
Job time: 32 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:53:49 ; Search time 40.16 Seconds
(without alignments)
499.847 Million cell updates/sec

Title: US-09-280-567-6

Perfect score: 1491

Sequence: 1 VAETPTVWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDSB/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1491	100.0	271	20	AA1980.DAT.*
2	1491	100.0	271	21	AA1981.DAT.*
3	1491	100.0	271	21	AA1982.DAT.*
4	1491	100.0	271	21	AA1983.DAT.*
5	1491	100.0	271	21	AA1984.DAT.*
6	1491	100.0	271	21	AA1985.DAT.*
7	1491	100.0	271	22	AA1986.DAT.*
8	1491	100.0	271	22	AA1987.DAT.*
9	1491	100.0	271	22	AA1988.DAT.*
10	1491	100.0	300	19	AA1989.DAT.*
11	1491	100.0	300	19	AA1990.DAT.*

12	1491	100.0	300	20	AA1991.DAT.*
13	1491	100.0	300	20	AA1992.DAT.*
14	1491	100.0	300	20	AA1993.DAT.*
15	1491	100.0	300	20	AA1994.DAT.*
16	1491	100.0	300	20	AA1995.DAT.*
17	1491	100.0	300	20	AA1996.DAT.*
18	1491	100.0	300	20	AA1997.DAT.*
19	1491	100.0	300	20	AA1998.DAT.*
20	1491	100.0	300	20	AA1999.DAT.*
21	1491	100.0	300	20	AA2000.DAT.*
22	1491	100.0	300	20	AA2001.DAT.*
23	1491	100.0	300	21	AA2002.DAT.*
24	1491	100.0	300	21	AA2003.DAT.*
25	1491	100.0	300	21	AA2004.DAT.*
26	1491	100.0	300	21	AA2005.DAT.*
27	1491	100.0	300	21	AA2006.DAT.*
28	1491	100.0	300	21	AA2007.DAT.*
29	1491	100.0	300	21	AA2008.DAT.*
30	1491	100.0	300	21	AA2009.DAT.*
31	1491	100.0	300	21	AA2010.DAT.*
32	1491	100.0	300	21	AA2011.DAT.*
33	1491	100.0	300	21	AA2012.DAT.*
34	1491	100.0	300	21	AA2013.DAT.*
35	1491	100.0	300	21	AA2014.DAT.*
36	1491	100.0	300	21	AA2015.DAT.*
37	1491	100.0	300	21	AA2016.DAT.*
38	1491	100.0	300	21	AA2017.DAT.*
39	1491	100.0	300	21	AA2018.DAT.*
40	1491	100.0	300	21	AA2019.DAT.*
41	1491	100.0	300	21	AA2020.DAT.*
42	1491	100.0	300	21	AA2021.DAT.*
43	1491	100.0	300	21	AA2022.DAT.*
44	1491	100.0	300	21	AA2023.DAT.*
45	1491	100.0	300	21	AA2024.DAT.*

ALIGNMENTS

RESULT 1

AA1980.DAT.*

ID AA1980.DAT.* standard; Protein; 271 AA.

XX

AC AA1980.DAT.*

XX

DT 17-DEC-1999 (first entry)

XX

DE Human mFLINT #1 protein sequence.

XX

KW Human; FLINT; mFLINT; OPC3; tumour necrosis factor receptor; FasL;
KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW reperfusion-associated injury; aplastic anaemia; differentiation;
KW growth; myelodysplastic syndrome; pancytopenic condition;
KW myocardial ischaemia.

XX

OS Homo sapiens.

XX

PN WO950413-A2.

XX

PD 07-OCT-1999.

XX

PF 30-MAR-1999; 99WO-US06797.

XX

PR 30-MAR-1998; 98US-0079856.

PR 20-MAY-1998; 98US-0086074.

PR 09-SEP-1998; 98US-0099643.

PR 17-DEC-1998; 98US-0112577.

PR 18-DEC-1998; 98US-0112703.

PR 22-DEC-1998; 98US-0113407.

XX

PA (ELIL) LILLY & CO ELI.

FT Misc-difference 169 /note= "optionally replaced with Ala"
 FT Misc-difference 171 /note= "optionally replaced with Asn"
 FT Misc-difference 172 /note= "optionally replaced with Asn"
 FT Misc-difference 179 /note= "optionally replaced with Thr"
 FT Misc-difference 183 /note= "optionally replaced with Lys"
 FT Misc-difference 194 /note= "optionally replaced with Asn"
 FT Misc-difference 196 /note= "optionally replaced with Thr"
 FT Misc-difference 209 /note= "optionally replaced with Thr"
 FT Misc-difference 225 /note= "optionally replaced with Arg"
 FT Misc-difference 237 /note= "optionally replaced with Glu"
 FT Misc-difference 270 /note= "optionally replaced with Gly"

W0200058465-A2.

05-OCT-2000.

20-MAR-2000; 2000WO-US06417.

30-MAR-1999; 99US-0126839.

21-JUN-1999; 99US-0140077.

21-JUN-1999; 99US-0140156.

20-OCT-1999; 99US-0160566.

18-FEB-2000; 2000US-0183398.

(ELIL) LILLY & CO ELI.

Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;

Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;

Wroblewski VJ;

WPI: 2000-656167/63.

N-PSDB; AAA75999.

FAS Ligand Inhibitory Protein analogs useful for treating abnormal apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis, chronic obstructive pulmonary disease ulcerative colitis or Crohn's disease

Claim 1: Page 112-113; 114pp: English.

The present sequence represents a mature human FAS Ligand Inhibitory Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature FLINT protein is modified to produce analogues, which have greater potency, longer in vivo half-lives, decreased aggregation, decreased absorption onto surfaces, increased solubility and improved ease of formulation. The FLINT analogue is useful for treating a patient suffering from disease or condition relating to abnormal apoptosis such as acute lung injury, acute respiratory distress syndrome, pulmonary fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or Crohn's disease.

Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 21; Length 271;

Best Local Similarity 100.0%; Pred. No. 4.6e-115;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPHDAETGRLVCAQCPCPTGVQPCRRSPPTCGPCPRHYTFQWNYLERCR 60

 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 vaetptyprdaetgerlvcaqcpcptgvqpcrrdspttcgpcprhytqfwnylcr 60

QY 61 YCNVLCGEREEERACHATHNRACRRTGFFAHAGFCLEHASCPPGAGVIAPPTPSONTQ 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 ycnvlcgerееееаrаchаthnrасrrtgffаhаgfclehasсppgаgvіаpgtpsntq 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 COPCPCTESASSSSFOCPHNCATGALANVPGSSSHDTICTCTGFPPLSTRVPGA 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 cqpсррtіsаssssfосрhncаtgаlаnvpгssshdtісtсtgfpplstrvpgae 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 ECERAVIDFVAFQDISIKRLQLQALEAPGEGWGPTRAGRAALQKLRRRLTELLGAQD 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 есerаvіdfvаfqдіsіkrlqlqаlеаpеgеwgpтраgгaаlqklrrrltеllgаqđ 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 GALLVRLQALRVARMPGLERSVRERPLPVH 271
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 gаllvrllqаlrvаrmpgllersvrerflpvh 271
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 3
 AAB19705
 ID AAB19705 standard; Protein; 271 AA.
 XX
 AC AAB19705;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Human FAS ligand inhibitor protein FLINT.
 XX
 KW FLINT: FAS ligand inhibitory protein; human; protease resistant;
 KW acute lung injury; acute respiratory distress syndrome;
 KW chronic obstructive pulmonary disease; pulmonary fibrosis;
 KW ulcerative colitis; therapy; organ transplantation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 218..219 /note= "cleaved by trypsin-like proteases"
 FT Misc-difference 34 /note= "optionally replaced by Arg, as given in
 FT Claims 10, 11, 13 and 14"
 FT Misc-difference 36 /note= "optionally replaced by Thr, as given in
 FT Claims 10, 11, 13 and 14"
 FT Misc-difference 132 /note= "optionally replaced by Asn, as given in
 FT Claim 12"
 FT Misc-difference 194 /note= "optionally replaced by Asn, as given in
 FT Claims 11 and 14"
 FT Misc-difference 196 /note= "optionally replaced by Thr, as given in
 FT Claims 11 and 14"
 FT Misc-difference 214 /note= "optionally replaced by any naturally
 FT occurring amino acid"
 FT Misc-difference 215 /note= "optionally replaced by any naturally
 FT occurring amino acid"
 FT Misc-difference 216 /note= "optionally replaced by any naturally
 FT occurring amino acid, preferably Pro as
 FT given in Claims 9 and 15"
 FT Misc-difference 217 /note= "optionally replaced by any naturally
 FT occurring amino acid, preferably Tyr as
 FT given in Claim 9"
 FT Misc-difference 218 /note= "optionally replaced by any naturally
 FT occurring amino acid, preferably Gln, Glu,
 FT Ala, Gly, Ser, Val, Tyr or Asn as given in
 FT Claims, 9, 10, 11, 12, especially Gln as
 FT given in Claims 13, 14, 15, 35 and 36"
 FT

Misc-difference 219 /note= "optionally replaced by any naturally occurring amino acid"

Misc-difference 220 /note= "optionally replaced by any naturally occurring amino acid"

Misc-difference 221 /note= "optionally replaced by any naturally occurring amino acid"

Misc-difference 222 /note= "optionally replaced by any naturally occurring amino acid"

WO200058466-A2.

05-OCT-2000.

20-MAR-2000; 2000WO-US06418.

30-MAR-1999; 99US-0126839.

21-JUN-1999; 99US-0140073.

04-AUG-1999; 99US-0147071.

20-OCT-1999; 99US-0160524.

21-OCT-1999; 99US-0160669.

20-DEC-1999; 99US-0172744.

26-JAN-2000; 2000US-0178184.

(ELIL) LILLY & CO ELI.

Micanovic R, Rathnachalam R, Witcher DR;

WPI; 2000-664925/64.

N-PSDB; AAA88730.

Novel protease resistant FAS ligand inhibitory protein analogues resistant to in vivo or in vitro proteolysis at amino acid position 218 of the mature protein, useful for treating autoimmune diseases -

Claim 1; Page 94-95; 100pp; English.

The present sequence is that of human FAS ligand inhibitory protein FLINT mature protein. FLINT is a tumour necrosis factor receptor homologue that binds FAS ligand, preventing its interaction with FAS. This interaction is implicated in runaway apoptosis and inflammatory disease. FLINT also binds to LIGHT, a membrane-bound ligand, which may play a role in immune modulation and apoptosis. The invention relates to novel FLINT analogues (see also AAB19706-09) that are resistant to proteolysis by trypsin-like proteases between positions 218 and 219 of the FLINT mature protein sequence. The analogues have amino acid substitutions in the region comprising amino acids 214-222, and may contain additional substitutions at residues 34, 36, 132, 134 and/or 196. Nucleic acids, vectors and transformed host cells for recombinant production of the analogues are claimed. FLINT cDNA (see AAA88730) is used as a template for introducing the required point mutations. The protease resistant FLINT analogues are used to prevent or treat acute lung injury, acute respiratory stress syndrome, ulcerative colitis, chronic obstructive pulmonary disease, pulmonary fibrosis, to inhibit T lymphocyte activation, and to facilitate organ preservation for transplantation (claimed).

Sequence 271 AA:

Query Match 100.0%; Score 1491; DB 21; Length 271;

Best Local Similarity 100.0%; Pred. No. 4.6e-115; Gaps 0;

Matches 271; Conservative 0; Mismatches 0; Indels 0;

QY 1 VAETPTYPWRDAETGERLVCACQPPGTFVQRCRRDSTTCGPPRHYTQFWNYLERCR 60

|||||

Db 1 vaetptywrdaetgerlvcacqppgtfvrpcrrdspttcgpprhytqfwnylercr 60

|||||

QY 61 YCNVLGEREEERACHATHNRACRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 120

Db 61 ycnvlgerereearachathnracrtgffahagfclhascppgagviapgtpsqntq 120

|||||

QY 121 CQCPPTGTFSSASSSSQCPHNCNTALGALNVPGSSSHDTLCTCTGFPPLSTRVPGAE 180

|||||

Db 121 cdcppgtfssasssseqcqhnrctalgalnvpssshdtlctctgfpplstrvpgae 180

|||||

QY 181 ECERAVIDFVAFQDISIKRLQLQALEAPEGWGPPPRAGRAALQKLRRRLTELLGAOD 240

|||||

Db 181 eceravidfvaqdisikrlqlqaleapegwgpppragraalqklrrrtelligaqd 240

|||||

QY 241 GALLVRLQALVARMPGLERSVRERFLPVH 271

|||||

Db 241 gallvrlqalrvarmpglersvrerflpvh 271

|||||

RESULT 4

AA97247

ID AAY97247 standard; Protein; 271 AA.

XX

AC AAY97247;

XX

DT 19-DEC-2000 (first entry)

DE

DE M68 TNF receptor related protein (mature protein).

XX

KW M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;

KW receptor; immune response; cell differentiation; ligand; cancer;

KW bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;

KW Grave's disease; idiopathic myxedema; autoimmune diabetes;

KW thrombotic thrombocytopenic purpura; multiple sclerosis;

KW liver diseases; autoimmune gastritis; ulcerative colitis;

KW glomerulonephritis; pulmonary fibrosis; heart failure;

KW atherosclerosis; aplastic anaemia; myelodysplastic syndromes;

KW osteoporosis; Alzheimers disease; Parkinsons disease; stroke;

KW myocardial infarction; human.

XX

OS Homo sapiens.

XX

PN WO2000046247-A1.

XX

PD 10-AUG-2000.

XX

PF 04-FEB-2000; 2000WO-US03037.

XX

PR 05-FEB-1999; 99US-0118902.

PR 20-DEC-1999; 99US-0172754.

XX

PA (MERI) MERCK & CO INC.

XX

PI Bai C;

XX

DR WPI; 2000-506066/45.

XX

PT Isolated human M68 nucleic acids and proteins which are part of the

PT tumor necrosis factor receptor (TNFR) family, useful for identifying

PT modulators that may be used to treat various diseases e.g. cancer,

PT osteoporosis, Alzheimer's disease

XX

PS Claim 1; Page 76; 80pp; English.

XX

CC The M68 protein is a member of a family of proteins which have

CC roles in immune responses, cell death, cell proliferation and

CC stimulation of cell differentiation. M68 lacks a transmembrane domain

CC and is a secreted factor suggesting that it functions as a natural

CC inhibitor for its ligand. The altered expression pattern of M68 in a

CC multitude of tissues suggests that M68 may play a role in cancer by

CC binding to its ligand and blocking apoptotic cell death induced by

CC such a ligand. This anti-apoptotic role of M68 suggests that

CC modulators of M68 will be useful in treatment of apoptosis-related

CC diseases such as various forms of cancer and various bone disorders.

CC M68 nucleic acids and proteins are therefore useful for treating

CC conditions involving atypical apoptosis and for identifying

modulators of M68. Modulators of M68 are useful for treatment of cancer and other diseases associated with abnormal levels of apoptosis including systemic lupus erythematosus, Hashimoto's thyroiditis, Grave's disease, idiopathic myxedema, autoimmune diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis, liver diseases, autoimmune gastritis, ulcerative colitis, glomerulonephritis, pulmonary fibrosis, heart failure, atherosclerosis, aplastic anaemia, myelodysplastic syndromes, osteoporosis, Alzheimer's disease, Parkinson's disease, stroke, and myocardial infarction.

Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 21; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.6e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTYPWRDAETGERLVCAQCPTGTFVQRCRRDSPTTCGPPRHYTFQWNYLERCR 60
|||||
Db 1 vaetptywrdaetgerlvcaqcpptgfvqrcrrdspttcgppprhytqfwnylerc 60

QY 61 YCNVLCGEREEERACHATHNRACRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120
|||||
Db 61 ycnvlgereearachathnrcrtgffahagfclehascpagviapgtpsqntq 120

QY 121 CQPCPGTFSASSSSSEQCPHNCRTALGLALNPVSSSHDTICTSGTGPLSTRVPGAE 180
|||||
Db 121 cqpcpgtfsasssseqcphnrcrtalglalnvpssshdtictctgfp1strvpgae 180

QY 181 ECERAVIDFVAFODISIKRLQLLQALEAPEGWGPTPRAGRAALQLKRLRLTELLGAQD 240
|||||
Db 181 ecearavidfvafodisikrlqlrlqaleapegwptpragraalqlkrrrlteligaqd 240

QY 241 GALLVRLQLALRVARMPGLERSVRERFLPVH 271
|||||
Db 241 gallvrlqlalrvarmpglersvrerflpvh 271

RESULT 5

AA96598
ID AA96598 standard; Protein; 271 AA.

AC- AA96598;

DT 26-SEP-2000 (first entry)

DE Human mature FLINT.

XX FLINT; osteoprotegerin 3; OPG3; tumour necrosis factor receptor; TNFR; FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic; anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic; anti-inflammatory; antibacterial; immunosuppressive.

OS Homo sapiens.

XX WO200037094-A2.

PN 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30734.

XX 22-DEC-1998; 98US-0113407.

PR 30-MAR-1999; 99WO-US06797.

PR 20-OCT-1999; 99US-0172239.

XX (ELIL) LILLY & CO ELI.

XX Cohen FU, Posada JA, Wierda D;

XX WPI; 2000-475441/41.

DR N-PSDB; AA51077.

XX

PT Use of mature FLINT for treating e.g. acute respiratory distress syndrome, ulcerative colitis or ischemic injury during organ transplantation
PT
XX Example 8; Fig 3; 125pp; English.

XX Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas mediated apoptotic and pro-inflammatory activity. mFLINT is useful for treating acute respiratory distress syndrome, treating or inhibiting ulcerative colitis, inhibiting ischemic injury during organ transplantation or for organ preservation during transplantation. mFLINT can also be used to treat acute liver failure, inflammation of the liver, abnormal (hepatocyte) apoptosis, sepsis, disorders associated with inflammation, hepatitis, ischemia, hypercoagulation or reperfusion, damage to a cardiac myocyte resulting from abnormal myocardial ischemia, Type I diabetes, cancer, damage to an innocent bystander tissue induced by a chemotherapeutic or therapeutic irradiation, aplastic anaemias, myelodysplastic syndromes and pancytopenic conditions.

XX Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 21; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.6e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTYPWRDAETGERLVCAQCPTGTFVQRCRRDSPTTCGPPRHYTFQWNYLERCR 60
|||||
Db 1 vaetptywrdaetgerlvcaqcpptgfvqrcrrdspttcgppprhytqfwnylerc 60

QY 61 YCNVLCGEREEERACHATHNRACRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120
|||||
Db 61 ycnvlgereearachathnrcrtgffahagfclehascpagviapgtpsqntq 120

QY 121 CQPCPGTFSASSSSSEQCPHNCRTALGLALNPVSSSHDTICTSGTGPLSTRVPGAE 180
|||||
Db 121 cqpcpgtfsasssseqcphnrcrtalglalnvpssshdtictctgfp1strvpgae 180

QY 181 ECERAVIDFVAFODISIKRLQLLQALEAPEGWGPTPRAGRAALQLKRLRLTELLGAQD 240
|||||
Db 181 ecearavidfvafodisikrlqlrlqaleapegwptpragraalqlkrrrlteligaqd 240

QY 241 GALLVRLQLALRVARMPGLERSVRERFLPVH 271
|||||
Db 241 gallvrlqlalrvarmpglersvrerflpvh 271

RESULT 6

AAE03567
ID AAE03567 standard; Protein; 271 AA.

XX AAE03567;

XX 04-AUG-2001 (first entry)

XX Human mature fas ligand inhibitory protein (FLINT).

XX Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
chronic renal failure; graft-vs-host disease; cutaneous inflammation;
vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
Down's syndrome; multiple sclerosis; cytostatic; neurotropic;
neuroprotective; vasotropic.

XX Homo sapiens.

OS

XX Key Location/Qualifiers
FH Modified-site 144
FT /note= "N-linked glycosylation site"
FT Modified-site 174
FT /note= "O-linked glycosylation site"
FT Modified-site 216
FT /note= "O-linked glycosylation site"
FT Cleavage-site 218..219
FT /note= "Proteolytic cleavage"
XX WO200142463-A1.
PN 14-JUN-2001.
XX 29-NOV-2000; 2000WO-US30166.
XX 07-DEC-1999; 99US-0169367.
PR 07-DEC-1999; 99US-0169381.
PR 07-DEC-1999; 99US-0169412.
PR 23-MAR-2000; 2000US-0191430.
XX (ELIL) LILLY & CO ELI.
XX Lu J, Witcher DR;
PI WPI; 2001-381684/40.
DR N-PSDB; AAD07380.
XX New FLINT polypeptide for treating and/or preventing acute lung injury,
PT acute respiratory distress syndrome, ulcerative colitis, and
PT graft-versus-host disease, comprises O-linked or N-linked
PT oligosaccharides -
XX
XX Example 1; Page 52-53; 60pp; English.
PS
XX The present sequence is human mature fas ligand inhibitory protein
CC (FLINT). FLINT, a homologue of tumour necrosis factor receptor
CC protein (TNFR), binds fas ligand (FasL) and thereby preventing the
CC interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC oligosaccharides is useful for preventing or treating acute lung injury
CC (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC to facilitate organ preservation for transplantation and to inhibit T
CC lymphocyte activation. FLINT is useful for treating and/or preventing
CC diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC host disease, cutaneous inflammation, vascular leak syndrome,
CC Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC psoriasis, Down's syndrome, and multiple sclerosis.
XX
SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.6e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VAETPTYPWRDAETGERLYCAQCPGCTFFVORPCRRDSPPTCGPPRHYTQFWNYLERCR 60
DB 1 vaetptyprdaetgerlyvcacqpgctfvgprccrrdspttcgpcprhytqfwnylcr 60
QY 61 YCNVLGGEREEERACHATHNACRCRTGFFAHAGFCLHASCPCPGAGVIAPGTPSQNTQ 120
DB 61 ycnvlcgereeeearachathnacrctrtgffahagfclhascppgagviapgtpsqntq 120
QY 121 CQCPPTGTFSSSSSEQCPHRNCTALGLALNVPGSSSHDTLCTSCGTGFLSTRVPGAE 180
DB 121 cqcpptgtfssssseqcqhnrnctalglnlalnvpssshdltctscgtgflstrvpgae 180

QY 181 ECERAVIDFAFODISIKRLQLLQALEAPEGWGPTPRAGRAALQKLRRRLTELGAQD 240
DB 181 eceravidfvaqdisikrlqlqaleapegwpgtppragraalqklrrrltellgaqd 240
QY 241 GALLYVLLQALVARMPGLERSVRERFLPVH 271
DB 241 gallvllqalrvarmpglersvrerflpvh 271
RESULT 7
AAB68044
ID AAB68044 standard; Protein; 271 AA.
XX
AC AAB68044;
XX
DT 29-JUN-2001 (first entry)
XX
DE Amino acid sequence of a human mature FLINT polypeptide.
XX
KW FLINT; Fas ligand inhibitory protein; divalent metal cation; Fas;
KW Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS Homo sapiens.
XX
PN WO200118055-A1.
XX
PD 15-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-US20807.
XX
PR 10-SEP-1999; 99US-0153339.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Atkinson PR, Tian Y, Witcher DR;
XX
DR WPI; 2001-273382/28.
XX
PT Compositions comprising a divalent metal cation and a Fas Ligand
PT Inhibitory protein (FLINT), for reducing or inducing aggregation of
PT FLINT and for treating diseases involving FasL/Fas and/or
PT LIGHT/T-beta-R receptor interactions -
XX
PS Example 1; Page 39-40; 44pp; English.
XX
CC The present sequence represents a mature FLINT (Fas Ligand Inhibitory
CC Protein) polypeptide. The specification describes a composition
CC comprising a divalent metal cation and FLINT protein. The composition
CC is used either for reducing, reversing or eliminating aggregation and
CC precipitation of FLINT or for inducing oligomerisation or aggregation
CC of FLINT molecules. They can be used for purifying FLINT and/or
CC maintaining FLINT in solution. The compositions are used to treat
CC and/or prevent disorders associated with the binding of Fas to FasL
CC and/or LIGHT to the TNFR and/or TR2/HVEM receptors. Uses include the
CC treatment of acute liver failure and cerebral ischemia and the prevention
CC of apoptosis.
XX
SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.6e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VAETPTYPWRDAETGERLYCAQCPGCTFFVORPCRRDSPPTCGPPRHYTQFWNYLERCR 60
DB 1 vaetptyprdaetgerlyvcacqpgctfvgprccrrdspttcgpcprhytqfwnylcr 60
QY 61 YCNVLGGEREEERACHATHNACRCRTGFFAHAGFCLHASCPCPGAGVIAPGTPSQNTQ 120
DB 61 ycnvlcgereeeearachathnacrctrtgffahagfclhascppgagviapgtpsqntq 120
QY 121 CQCPPTGTFSSSSSEQCPHRNCTALGLALNVPGSSSHDTLCTSCGTGFLSTRVPGAE 180

```

Db 121 cpcp pgtfsas sssseqcqhnrctalgalnvp gssshdtlctctctgffplstrvpgae 180
      |||
QY 181 ECERAVIDFAVDQISIKRLQRLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 240
      |||
Db 181 eceravidfvaqdisikrlqrlqaleapegwptpragraalqklrrrltellgaqd 240
      |||
QY 241 GALLVRLQALRVARMPGLERSVRERFLPVH 271
      |||
Db 241 gallvrlqalrvarmpglersvrerflpvh 271
      |||

RESULT 8
AAB68047
ID AAB68047 standard; Protein; 271 AA.
XX
AC AAB68047;
XX
DT 29-JUN-2001 (first entry)
XX
DE Amino acid sequence of a human mature FLINT polypeptide.
XX
KW FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS Homo sapiens.
XX
PN WO200118041-A2.
XX
PD 15-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-US20805.
XX
PR 10-SEP-1999; 99US-0153445.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Atkinson PR, Tian Y, Witcher DR;
XX
DR WPI; 2001-273381/28.
XX
CC Compositions comprising a divalent metal cation and a FAS Ligand
PT Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT FLINT and for treating diseases involving FasL/Fas and/or
PT LIGHT/LT-beta-R receptor interactions -
XX
PS Disclosure; Page 30-31; 33pp; English.
XX
CC The present sequence represents a human mature FLINT (FAS Ligand
CC Inhibitory Protein) polypeptide. The specification describes a
CC composition comprising a divalent metal cation and FLINT protein. The
CC aggregation is used either for reducing, reversing or eliminating
CC aggregation and precipitation of FLINT or for inducing oligomerisation
CC or aggregation of FLINT molecules. They can be used for purifying FLINT
CC and/or maintaining FLINT in solution. The compositions are used to treat
CC and/or prevent disorders associated with the binding of Fas to FasL
CC and/or LIGHT to the LTbetar and/or TR2/HVEM receptors. Uses include the
CC treatment of acute liver failure and cerebral ischemia and the prevention
CC of apoptosis.
XX
SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.6e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPRDAETGERLVCAQCPGCTFVQRCRRDSPPTCGPPRHYTQFWNYLERCR 60
      |||
Db 1 vaetptyprdaetgerlvcaqcpptfvgprcrrdspttcgpprhytqfwnylercr 60
      |||
QY 61 YCNVLGGEREEEARACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
      |||
Db 61 ycnvlgerereearachathnracrtgffahagfclehascpaggviapgtpsqntq 120
      |||
QY 121 CQPCPGTFSASSSSEQCQPHNRCTALGLALNVP GSSSHDTLCTCTCTGFFPLSTRVPGAE 180
      |||

```

```

Db 61 ycnvlgerereearachathnracrtgffahagfclehascpaggviapgtpsqntq 120
      |||
QY 121 CQPCPGTFSASSSSEQCQPHNRCTALGLALNVP GSSSHDTLCTCTCTGFFPLSTRVPGAE 180
      |||
Db 121 cpcp pgtfsas sssseqcqhnrctalgalnvp gssshdtlctctctgffplstrvpgae 180
      |||
QY 181 ECERAVIDFAVDQISIKRLQRLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 240
      |||
Db 181 eceravidfvaqdisikrlqrlqaleapegwptpragraalqklrrrltellgaqd 240
      |||
QY 241 GALLVRLQALRVARMPGLERSVRERFLPVH 271
      |||
Db 241 gallvrlqalrvarmpglersvrerflpvh 271
      |||

RESULT 9
AAB74465
ID AAB74465 standard; protein; 271 AA.
XX
AC AAB74465;
XX
DT 30-MAY-2001 (first entry)
XX
DE Human FLINT mature protein.
XX
KW Human; FLINT; FAS ligand inhibitory protein; analogue; apoptosis;
KW inflammatory disease.
XX
OS Homo sapiens.
XX
PN WO200118202-A2.
XX
PD 15-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-US20806.
XX
PR 10-SEP-1999; 99US-0153433.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Atkinson PR, Tian Y, Witcher DR;
XX
DR WPI; 2001-257796/26.
XX
PT Compositions useful for reducing/inducing aggregation of a FLINT analog
PT comprise a divalent metal cation and a protease-resistant FAS Ligand
PT Inhibitory Protein (FLINT) analog -
XX
PS Claim 4; Page 41-42; 44pp; English.
XX
CC The present invention describes a composition comprising a divalent metal
CC cation associated with a protease resistant Fas ligand inhibitory protein
CC (FLINT) analogue. The composition is useful in the treatment of diseases
CC associated with Fas binding to its ligand, such as acute liver failure,
CC inflammatory diseases, cerebral ischaemia and apoptosis. The present
CC sequence is the mature FLINT protein.
XX
SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.6e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPRDAETGERLVCAQCPGCTFVQRCRRDSPPTCGPPRHYTQFWNYLERCR 60
      |||
Db 1 vaetptyprdaetgerlvcaqcpptfvgprcrrdspttcgpprhytqfwnylercr 60
      |||
QY 61 YCNVLGGEREEEARACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
      |||
Db 61 ycnvlgerereearachathnracrtgffahagfclehascpaggviapgtpsqntq 120
      |||
QY 121 CQPCPGTFSASSSSEQCQPHNRCTALGLALNVP GSSSHDTLCTCTCTGFFPLSTRVPGAE 180
      |||

```



```

SQ      Sequence      300 AA;

Query Match      100.0%; Score 1491; DB 19; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.2e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VAETPTYPWRDAETGERLVCAQCPPGTFVORPCRRDSTTCGPPRHYTOFWNYLERCR 60
      |||||||
Db      30 vaetptypwrdaetgerlvcaqcpptfvqrrdspttcgpprhytqfwnylcr 89

QY      61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
      |||||||
Db      '90 ycnvlgereeeearachathnrcrctgffahagfclehascpaggviapgtpsqntq 149

QY      121 CQPCPGTFSASSSSQCPHNRCTALGLALNVPGSSSHDTCTSGTPLSTRVPGA 180
      |||||||
Db      150 cqpccpgtfsasssseqcphnrctalgialnvpgssshdtctsgtgpflstrvpgae 209

QY      181 ECRRAVIDFVAFODISIKRLQRLLOALEAPGCGPTPRAGRAALQKLRRRLTELLGAQD 240
      |||||||
Db      210 eceravidfvafqdisikrlqrlloaleapegwgptpragraalqlkrrrltellgaqd 269

QY      241 GALLVRLQLALRVARMPGLERSVRERFLPVH 271
      |||||||
Db      270 gallvrlqlalrvarmpglrsvrerflpvh 300

RESULT 12
AAY03099
ID      AAY03099 standard; Protein; 300 AA.
AC
AC      AAY03099;
DT
DT      09-DEC-1999 (first entry)
XX
XX      Human lung TNF-receptor protein.
DE
DE      Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;
KW      detection; immunoassay; diagnosis; disease; immune system; tumour;
KW      osteogenic system; cardiovascular system; central nervous system; asthma;
KW      peripheral nervous systems; transplant incompatibility; antitumor;
KW      rheumatoid arthritis; antiasthmatic; antiarthritic.
XX
OS
OS      Homo sapiens.
FH
FH      Key
FT      CDS
FT      134..1036
FT      /*tag= a
FT      /product= "TNF-receptor"
XX
XX      DE19809978-A1.
XX
XX      16-SEP-1999.
XX
XX      09-MAR-1998; 98DE-1009978.
XX
XX      09-MAR-1998; 98DE-1009978.
XX
XX      (BADI ) BASF AG.
XX
XX      Kroeger B;
XX
XX      WPI: 1999-519473/44.
XX
XX      N-PSDB; AA209998.
XX
XX      New soluble member of tumor necrosis factor receptor family, useful for
PT      identification specific modulators and for treating disease e.g. tumors
PT
PT
XX
XX      Claim 1; Page 8-9; 10pp; German.
PS
PS      This invention describes a novel tumour necrosis factor (TNF) receptor .
XX
XX      CC

```

(I) isolated from human lung tissue. (I) is used: (i) to raise specific antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands (A), potential therapeutic agents; and (iii) therapeutically (optionally) expressed from a gene therapy vector) in conditions associated with a deficit of (I). Ab are used: (a) for qualitative or quantitative detection of (I) in standard immunoassays (for diagnosis of disease, or susceptibility, or for monitoring); and (b) as therapeutic inhibitors in cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is used: (A) for recombinant production of (I); (B) also its oligonucleotide fragments, in standard hybridization and/or amplification assays; (C) as source of antisense molecules or ribozymes; and (D) to produce transgenic animals (for studying (patho)physiology of (I)). Diseases possibly associated with under- or over-expression of (I) are those of the immune, osteogenic, cardiovascular and central or peripheral nervous systems, tumors, transplant incompatibility, asthma and rheumatoid arthritis. The products of the invention have antitumor, antiasthmatic and antiarthritic activity. This sequence represents the TNF-receptor of the invention.

Query Match 100.0%; Score 1491; DB 20; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.2e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPPGTFVORPCRRDSTTCGPPRHYTOFWNYLERCR 60
|||||
Db 30 vaetptypwrdaetgerlvcaqcpptfvqrrdspttcgpprhytqfwnylcr 89

QY 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
|||||
Db 90 ycnvlgereeeearachathnrcrctgffahagfclehascpaggviapgtpsqntq 149

QY 121 CQPCPGTFSASSSSQCPHNRCTALGLALNVPGSSSHDTCTSGTPLSTRVPGA 180
|||||
Db 150 cqpccpgtfsasssseqcphnrctalgialnvpgssshdtctsgtgpflstrvpgae 209

QY 181 ECRRAVIDFVAFODISIKRLQRLLOALEAPGCGPTPRAGRAALQKLRRRLTELLGAQD 240
|||||
Db 210 eceravidfvafqdisikrlqrlloaleapegwgptpragraalqlkrrrltellgaqd 269

QY 241 GALLVRLQLALRVARMPGLERSVRERFLPVH 271
|||||
Db 270 gallvrlqlalrvarmpglrsvrerflpvh 300

RESULT 13
AAY42182
ID AAY42182 standard; Protein; 300 AA.
XX
AC AAY42182;
XX
DT 17-DEC-1999 (first entry)
XX
XX Human FLINT #1 protein sequence.
XX
KW Human; FLINT; mFLINT; OPC3; tumour necrosis factor receptor; FasL;
KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW reperfusion-associated injury; aplastic anaemia; differentiation;
KW growth; myelodysplastic syndrome; pancytopenic condition;
KW myocardial ischaemia.
XX
OS Homo sapiens.
XX
XX WO9950413-A2.
XX
XX 07-OCT-1999.
XX
XX 30-MAR-1999; 99WO-US06797.
XX
XX 30-MAR-1998; 98US-0079856.

PR 20-MAY-1998; 98US-0086074.
 PR 09-SEP-1998; 98US-0099643.
 PR 17-DEC-1998; 98US-0112577.
 PR 18-DEC-1998; 98US-0112703.
 PR 18-DEC-1998; 98US-0112933.
 PR 22-DEC-1998; 98US-0113407.
 XX (ELIL) LILLY & CO ELI.
 PA Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
 PI Hui KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
 PI Song HY, Wang J, Wu X, Zuckerman SH;
 XX WPI: 1999-591319/50.
 DR N-PSDB; AA225375.
 XX Use of mature FLINT for treating acute liver failure, inflammation,
 PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
 PT and proinflammatory activity
 XX Claim 30; Fig 1; 99pp; English.
 PS The present invention describes therapeutic applications of mature FLINT
 XX (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
 CC (mFLINT), which is a member of the tumour necrosis factor receptor
 CC superfamily, is used for treating acute liver failure, inflammation of
 CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
 CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
 CC injury or disorder such as hypercoagulation (including use with
 CC thrombolytic or anti-thrombolytic agents); reperfusion-associated injury
 CC or disorder, type I diabetes, cancer, cell damage or damage to an
 CC innocent bystander tissue that is induced by a chemotherapeutic agent or
 CC therapeutic irradiation, treating haematopoietic progenitor cells that
 CC have been exposed to therapeutic radiation or chemotherapy, aplastic
 CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
 CC also used for promoting the growth or differentiation of a haematopoietic
 CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
 CC resulting from abnormal myocardial ischaemia. The present sequence
 CC represents human FLINT.
 XX Sequence 300 AA;
 SQ

Query Match 100.0%; Score 1491; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 5.2e-115;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPTGTFVQPCRRDSPTTCGCPPRHYTQFWNYLERCR 60
 Db |||||
 30 vaetpypwrdaetgerlvcaqcptgtfvqpcrrdspttcgcpprhytqfwnylercr 89
 QY 61 YCNVLGGEREEARACHATHNRACRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 120
 Db |||||
 90 ycnvlcgereearachathnrcrctgffahagfclhascppgagviapgtpsqntq 149
 QY 121 CQCPPTGTSASSSSSEQCPHNCRTALGLALNVPSSSHDTLCTSGTGPPLSTRVPGAE 180
 Db |||||
 150 cqcpptgttsassssseqcqhncrtalglalnvpssshdtlctsgtgpplstrvpgae 209
 QY 181 ECERAVIDFVAFODISTKRLQLLQALEAPEGWGPTPRAGRAALQLKLRRLTELLGAQD 240
 Db |||||
 210 eceravidfvafodisikrlqllqaleapegwptpragraalqlklrrltellgaqd 269
 QY 241 GALLVRLQALVARMPGLERSVRERFLPVH 271
 Db |||||
 270 gallvrlqalvarmpglersvrerflpvh 300

RESULT 14
 AAY17479
 ID AAY17479 standard; Protein; 300 AA.
 XX
 AC AAY17479;

XX 02-AUG-1999 (first entry)
 DT Mammalian tumour necrosis factor receptor OPG-2.
 XX
 DE Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease;
 XX osteopenic disorder; osteoclast activity; primary osteoporosis;
 KW hyperglycaemia; osteolytic metastasis; immune response; cancer.
 XX
 OS Mammalia.
 XX
 PN WO9926977-A1.
 XX
 PD 03-JUN-1999.
 XX
 XX 24-NOV-1998; 98WO-US25065.
 PF
 XX 17-FEB-1998; 98US-0074896.
 PR
 PR 24-NOV-1997; 97US-0066446.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Tschopp J;
 XX
 DR WPI: 1999-347693/29.
 DR N-PSDB; AAX76052.
 XX
 PT New tumour necrosis factor family receptor OPG-2
 XX
 PS Claim 1; Page 18; 22pp; English.
 CC The present sequence represents a mammalian tumour necrosis factor
 CC receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis
 CC factor receptor family, and can be used: (i) to raise specific with
 CC antibodies (Ab), (ii) to treat osteopenic disorders associated with
 CC excessive osteoclast activity, e.g. primary osteoporosis, Paget's
 CC disease, hyperglycaemia of malignancy, or osteolytic metastases; (iii)
 CC for affinity purification of cognate ligands, and (iv) to screen for
 CC ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents
 CC such as soluble forms of the protein, are used to prevent, or reduce
 CC severity of, an immune response, and for treating cancer. They can also
 CC be used in diagnostic assays. The nucleic acid sequence encoding OPG-2
 CC can be used as a probe to isolate related sequences from other species.
 XX
 SQ Sequence 300 AA;

Query Match 100.0%; Score 1491; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 5.2e-115;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPTGTFVQPCRRDSPTTCGCPPRHYTQFWNYLERCR 60
 Db |||||
 30 vaetpypwrdaetgerlvcaqcptgtfvqpcrrdspttcgcpprhytqfwnylercr 89
 QY 61 YCNVLGGEREEARACHATHNRACRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 120
 Db |||||
 90 ycnvlcgereearachathnrcrctgffahagfclhascppgagviapgtpsqntq 149
 QY 121 CQCPPTGTSASSSSSEQCPHNCRTALGLALNVPSSSHDTLCTSGTGPPLSTRVPGAE 180
 Db |||||
 150 cqcpptgttsassssseqcqhncrtalglalnvpssshdtlctsgtgpplstrvpgae 209
 QY 181 ECERAVIDFVAFODISTKRLQLLQALEAPEGWGPTPRAGRAALQLKLRRLTELLGAQD 240
 Db |||||
 210 eceravidfvafodisikrlqllqaleapegwptpragraalqlklrrltellgaqd 269
 QY 241 GALLVRLQALVARMPGLERSVRERFLPVH 271
 Db |||||
 270 gallvrlqalvarmpglersvrerflpvh 300

RESULT 15

AA06817
ID AAY06817 standard; Protein; 300 AA.

XX
AC AAY06817;

XX
DT 24-JUN-1999 (first entry)

XX
DE Human Dcr3 polypeptide.

XX
KW Dcr3 polypeptide; tumour necrosis factor receptor; TNFR; Fas ligand;
KW apoptosis; T cell mediated immune response; allergy; asthma; cancer;
KW rheumatoid arthritis; Crohn's disease; guest vs. host disease; human;
KW gene therapy.

XX
OS Homo sapiens.

XX
PN WO9914330-A1.

XX
PD 25-MAR-1999.

XX
PF 18-SEP-1998; 98WO-US19661.

XX
PR 30-JUL-1998; 98US-0094640.

PR
18-SEP-1997; 97US-0059288.

XX
PA (GETH) GENENTECH INC.

XX
PI Ashkenazi AJ, Botstein D, Dodge KH, Goddard A, Gurney AL;
PI Kim KJ, Lawrence DA, Pitti R, Roy MA, Tumas DB;
PI Wood WI;

XX
DR WPI: 1999-244032/20.
DR N-PSDB; AAX32744.

PT
Dcr3 polypeptide related to tumor necrosis factor receptor

XX
PS Claim 5; Fig 1; 88pp; English.

XX
PS This represents a human Dcr3 polypeptide, a homologue of tumour necrosis
CC factor receptor (TNFR) polypeptide. Host cells containing a vector
CC comprising the Dcr3 nucleic acid can be used for the recombinant
CC expression of the protein. Dcr3 binds to Fas ligand, so it (or its
CC chimeras) are useful for modulating apoptosis in mammalian cells, also
CC other Fas-ligand induced activities, particularly to inhibit T cell
CC mediated immune responses, e.g. in treatment of allergy, asthma,
CC rheumatoid arthritis, Crohn's disease, guest vs. host disease etc. Dcr3
CC may also be used to identify specific binding proteins, potential
CC inhibitors. Antibodies against Dcr3 are used to treat cancer,
CC specifically of the lung and colon, also in diagnosis and for affinity
CC purification of the protein. Detecting mutations in the gene for Dcr3 is
CC also used to diagnose cancer, or predisposition to it. Dcr3 nucleic acid
CC is useful as hybridization probe to detect genomic or related sequences;
CC for chromosome and gene mapping; as source of antisense sequences; for
CC expression of recombinant Dcr3 and to generate transgenic animals (for
CC development and screening of therapeutic agents), also for in vivo or
CC ex vivo gene therapy.

XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1491; DB 20; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.2e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLYCAQCPGTFFVQRCRRDSPPTTCGPPRHYTFQWNYLERCR 60
|||||
DB 30 vaetptywrdaetgerlyvcaqcpgtffvqrcrrdspttcgpprhytqfwnylercr 89
|||||
QY 61 YCNVLGGEREEERACHATHNRACRGTFFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
|||||
DB 90 ycnvlgereeeearachathnrcrctgffahagfclehascpaggviapgtpsqntq 149
|||||
QY 121 CQPCPPTFSASSSSSEQCPHRNCTALGLALNVPSSSHDTLCTCTGTFPLSTRVPGAE 180

Db 150 cqcpcpptfsassssseqcqhncntalglalnvpssshdtlctctgfpplstrvpgae 209
|||
QY 181 ECERAVIDFVAFQDISIKRLQRLQLALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 240
|||||
DB 210 eceravidfvafqdisikrlqrlqlaleapegwptpragraalqklrrrltellgaqd 269
|||||
QY 241 GALLVRLQLALRVARMVPGLETSVRERFLPVH 271
|||||
DB 270 gallvrlqlalrvarmvpglersvrerflpvh 300
|||||

Search completed: May 10, 2002, 10:53:50
Job time: 79 sec

THIS PAGE BLANK (USPTO)